

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: October 3, 2002, 15:38:38 ; Search time 53.39 Seconds

(without alignments)
667.816 Million cell updates/secTitle: US-09-945-182-26
Perfect score: 1757

Sequence: 1 NSDLSHTPLRQKLFDVSM.....GNNVVVKQYEDMVVESCGCR 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

All number of hits satisfying chosen parameters: 747574

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802:*

- 1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
- 9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
- 10: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
- 16: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
- 17: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
- 18: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

RESULT 1

ID AAR78730 standard; Protein; 321 AA.

XX AAR78730;

AC AAR78730;

DT 30-NOV-1995 (first entry)

XX Human mature VL-1 (BMP-13) encoding sequence.

XX Bone morphogenetic protein; VL-1; tendon; ligament; tendinitis.
XX Homo sapiens.

XX Key Location/Qualifiers

1..201

202..321

FT Peptide /label= "mature protein
/note= "claimed"FT Misc-difference /note= "claimed"
/note= "claimed"

FT Misc-difference 202..321

FT Misc-difference 220..321

SUMMARIES

8

Result No.	Score	Query	Match	Length	DB ID	Description
1	1757	100.0	321	16	AAR78730	Human mature VL-1
2	1757	100.0	321	18	AAW26591	Human bone morphog Human full length
3	1757	100.0	321	22	AAE10982	Human growth/diffe Cartilage-derived
4	1747	99.4	455	22	AAM50216	Murine mv2 protein Murine BMP-13 homo Murine partial mv2
5	1368	77.9	436	17	AAP95636	TGF-beta-like clon New TGF-beta famil Human MP52. Homo
6	1207.5	68.7	263	16	AAR78739	
7	1207.5	68.7	263	18	AAP26595	
8	1202.5	68.4	263	22	AAE10985	
9	771	43.9	401	14	AAK40805	
10	771	43.9	501	16	AAW69600	
11	771	43.9	501	18	AAW36100	

(GEMY) GENETICS INST INC.

12	771	43.9	501	18	AAW19210	Human TGF-beta pro Human high mol. wt Human MP52 protein Human bone morphog TGF-beta superfami Human MP52. Homo Human bone morphog Human bone morphog Human bone morphog Human bone morphog Amino acid sequenc Cartilage-derived Human growth diffe Human TGF-beta MP5 GDF-6. Mus sp. A Murine growth diff Human bone morphog Human bone morphog Human bone morphog Murine mv1 protein Murine BMP-12 homo Murine partial mv1 Novel human diagno Fusion of BMP-2 pr BMP-2 propeptide/B Human BMP2 propept Human CDMP-2/GDF-6 Human CDMP-2/GDF-6 Murine GDF-6 finger Murine GDF-6, SEQ Mouse GDF-6 amino GDF-6 finger-1-hee Bovine CDMP-2, SE Bovine CDMP-2 amin Murine CDMP-2/GDF-6 Human CDMP-2/GDF-6
13	771	43.9	501	18	AAW11300	
14	771	43.9	501	18	AAW01799	
15	771	43.9	501	18	AAW12770	
16	771	43.9	501	19	AAW44868	
17	771	43.9	501	19	AAW33008	
18	765	43.5	388	18	AAW26592	
19	765	43.5	388	22	AAB610986	
20	765	43.5	388	22	AAB66867	
21	765	43.5	495	22	AAB60022	
22	765	43.5	495	22	AAB84550	
23	762	43.4	501	17	AAR56355	
24	762	43.4	501	21	AAY92034	
25	760	43.3	501	22	AAB70529	
26	731	41.6	134	16	AAR66867	
27	731	41.6	134	21	AAB12946	
28	691.5	39.4	294	16	AAR78729	
29	691.5	39.4	294	18	AAW26589	
30	691.5	39.4	294	22	AAB10912	
31	618	35.2	240	16	AAR78738	
32	618	35.2	240	18	AAW26594	
33	618	35.2	240	21	AAB09554	
34	601	34.2	184	22	AAB29375	
35	584	33.2	411	16	AAR78740	
36	584	33.2	411	18	AAW26597	
37	584	33.2	411	21	AAB02821	
38	575	32.7	102	21	AAB09556	
39	575	32.7	102	21	AAB02820	
40	575	32.7	102	21	AAY92579	
41	572	32.6	102	21	AAB09555	
42	572	32.6	102	21	AAB02821	
43	572	32.6	102	21	AAY92580	
44	563	32.0	102	21	AAB09556	
45	563	32.0	102	21	AAB02822	

ALIGNMENTS

Database :	A_Geneseq_032802:*	RESULT 1
ID	AAR78730	standard; Protein; 321 AA.
XX		
AC	AAR78730;	
DT	30-NOV-1995 (first entry)	
XX	Human mature VL-1 (BMP-13) encoding sequence.	
XX	Bone morphogenetic protein; VL-1; tendon; ligament; tendinitis.	
XX	Homo sapiens.	
XX	Key Location/Qualifiers	
FT	1..201	
FT	202..321	
FT	Peptide /label= "mature protein /note= "claimed"	
FT	Misc-difference /note= "claimed"	
FT	Misc-difference 202..321	
FT	Misc-difference 220..321	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1757	100.0	321	16	AAR78730	Human mature VL-1
2	1757	100.0	321	18	AAW26591	Human bone morphog Human full length
3	1757	100.0	321	22	AAE10982	Human growth/diffe Cartilage-derived
4	1747	99.4	455	22	AAM50216	Murine mv2 protein Murine BMP-13 homo Murine partial mv2
5	1368	77.9	436	17	AAP95636	TGF-beta-like clon New TGF-beta famil Human MP52. Homo
6	1207.5	68.7	263	16	AAR78739	
7	1207.5	68.7	263	18	AAP26595	
8	1202.5	68.4	263	22	AAE10985	
9	771	43.9	401	14	AAK40805	
10	771	43.9	501	16	AAW69600	
11	771	43.9	501	18	AAW36100	

Qy	241	PLEYEAYHCEGVYCDFFPLRSHLEPTNHAIOTLMNSMDPGSTPPSCVPIKLTPIISLYID	300	XX	Sequence	321 AA;
Db	241	pleyeayhcegvcdffplrshleptnhaiotlmnsmdpgstppscvcvptkltpislyid	300	Query Match Score 1757; DB 22;	Best Local Similarity 100.0%;	Pred. No. 8 2e-149;
ID	AAE10982	standard; Protein; 321 AA.		Mismatches 0;	Indels 0;	Gaps 0;
XX						
XX	18-DEC-2001	(first entry)				
XX		Human full length VL-1 or BMP-13 protein.				
DN						
AC	AAE10982;					
XX						
Human	bone morphogenic protein; BMP-13; vulnerability; antiinflammatory; analgesic; gene therapy; transforming growth factor-beta; TGF-beta; tissue formation; wound healing; tissue repair; ligament defect; VL-1; carpal tunnel syndrome; tendonitis.					
KW						
KW						
XX		Homo sapiens.				
Key		Location/Qualifiers				
FI	1..201	/label= signal_peptide				
FT	202..321	/label= Mature_BMP_12_protein				
FT						
OS						
XX						
PN	US6284872-B1.			RESULT 4		
XX				AAM5216		
PD	04-SEP-2001.			ID AAM5216 standard; Protein; 455 AA.		
XX				XX		
PF	28-FEB-1997;	97US-0808324.		AC AAM50216;		
XX				XX		
PR	22-DEC-1994;	94US-0362670.		DT 07-JAN-2002 (first entry)		
PR	07-DEC-1993;	93US-0164103.		XX		
PR	25-MAR-1994;	94US-0217780.		DE Human growth/differentiation factor-6-like protein AMF10.		
PR	02-NOV-1994;	94US-0333576.		XX		
XX				KW AMF10; human; growth/differentiation factor-6; cancer; cell proliferation; astrocytoma; glioma; therapy; diagnosis.		
PA	(GEMY) GENETICS INST INC.			XX		
PA	(HARD) HARVARD COLLEGE.			OS Homo sapiens.		
XX				XX		
Celeste AJ,	Wozney JM,	Rosen VA,	Wolfman NM,	FH Key		
Melton DA;			Thomsen GH;	Peptide 1..22	Location/Qualifiers	
DR	WPI: 2001-588978/66.			FT /label= Signal_peptide		
N-PSDB;	AAD18333.			FT 23..455		
XX				FT /label= Mature_protein		
PT	New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects, comprises DNA encoding propeptide linked to DNA encoding bone morphogenetic proteins (BMP) -12, BMP-13 or MP52 -			PN WO200174897-A2.		
PT	Example 1; Column 57-60; 42pp; English.			XX 11-OCT-2001.		
XX				XX 03-APR-2001; 2001WO-US10892.		
CC	The invention relates to a chimeric DNA comprising a DNA sequence encoding a propeptide from a member of the transforming growth factor (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence encoding an amino acid sequence encoding a mature polypeptide consisting of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA sequences are useful for producing proteins which induce tendon/ligament like tissue formation, and for isolating and cloning further DNA sequences encoding BMP-12 related proteins with similar activity. The proteins are useful for the induction of tendon/ligament-like tissue formation, wound healing, ligament and other tissue repair, augmenting the activity of bone morphogenetic proteins, and for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects. The present sequence is human VL-1 protein also designated as BMP-13.			XX 03-APR-2000; 2000US-194314P.		
CC				PR 16-AUG-2000; 2000US-225693P.		
CC				PA (CURAGEN CORP.		
CC				XX Vernet CAM, Burgess CE, Fernandes E, Taupier RJ, Quinn KE;		
CC				PI Spytek KA, Rastelli L, Herrmann JL;		
CC				XX DR 2001-626395/72.		
CC				DR N-PSDB; AAT17023.		
CC	New AMF1-10 polypeptides and encoding polynucleotides, useful for treating or preventing disorders related to modulation of cell			XX		
CC				PT		
CC				PT		

movement, cell signal processing, cell adhesion or migration pathways

PT e.g., cancer -
 PT movement, cell signal processing, cell adhesion or migration pathways
 XX
 PS Claim 1; Page 44-45; 134pp; English.

XX
 CC The present sequence is that of the novel, secreted human growth/differentiation factor-6 (GDF6)-like protein, AMF10. CC AMF10 is expressed in astrocytoma and glioma-derived tissue. DNA encoding the AMF8 may be useful in gene therapy, and the protein may also be used as a therapeutic, especially in treatment of cancer and other cell proliferative disorders. Generally, the AMF10 (AMFX) nucleic acids and proteins of the invention are useful for treating or preventing AMFX-associated disorders, e.g. a disorder related to cell signal processing and metabolic pathway modulation, cell adhesion or migration, pathway modulation, chemoresistance, radiotherapy resistance, survival in trophic factor limited secondary tissue site microenvironments, connective tissue disorders, tissue remodeling, oncogenesis, cancer of the breast, ovary, cervix, prostate, endometrium, stomach, colon, lung, bladder, kidney, brain, and soft-tissue, cellular transformation, development, tissue remodeling, inflammation, blood clot formation and resorption, haemopoiesis, angiogenesis, multidrug resistance related to organic anion transporters, malignant disease progression, autoimmunity and paracrine regulation of cell growth, and cellular responses to external stimuli, and other diseases, disorders, etc. (all claimed). AMFX Proteins are also used for screening drugs or compounds that modulate AMFX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of AMFX protein.

XX
 Sequence 455 AA;

Query Match 99.4%; Score 174; DB 22; Length 455;
 Best Local Similarity 100.0%; Pred. No. 9.8e-148;
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DISHTPLRQKYLFDVMSLSDKEELVGAELLFRQAPSAPNGPAGPLHVLFCPLSPLL 62
 Db 137 dlshtplrkqylfdvmsldeelvgaellfrqapsapngpagsplhvlfcplsppl 196
 .Qy 63 LDARTLDQPGAPPAGWENFDWQGLRHOPWKOLCLEDRAWGELDAGEEARARGQQPP 122
 Db 197 ldartldqpgappagwefdwqglrhopwkolkledrawgeldageearargqqpp 256
 Qy 123 PPDLRSLGFGRRYRPPQERALLVFTRSORKNLNAEMREOLGSAFAAGPGAGAEWSWPPP 182
 Db 257 ppdlrslgfgrryrrpperallvftrsqrnlfaamreqigssaaagpagaeswppp 316
 .Qy 183 SGADPAREWLPSGPGRERRRTAFASRHKRGKKSRERCSKKPLHVNFEKGWDWIIAPL 242
 Db 317 sgadparwlpsgpgrerrrtatascrigkksrlrcskpk1vnfk1gwdwiaipl 376
 Qy 243 EYAYHCBGVCDPLRSHLEPTNHAIIQTLMNSMDGSTPPSCCVPTKLTPISTLYIDAG 302
 Db 377 eyeayheegdfpirshleptnhaiqtimsmopstppscvcptkitpisslyidag 436
 Qy 303 NNVVYKOEDMYVESCGCR 321
 Db 437 nnvvkydoyedmvvescgr 455

RESULT 5
 AA95636 standard; Protein; 436 AA.
 XX
 AC
 XX
 DT 25-OCT-1996 (first entry)
 DE Cartilage-derived morphogenetic protein-2.
 XX
 KW Cattle; cartilage-derived morphogenetic protein-2; CDMP-2;
 KW

KW articular cartilage; chondrogenic; vulnerability; implantation;
 KW chondromalacia; osteoarthritis; therapy; joint repair.
 XX
 OS Bos taurus.
 XX
 Key Location/Qualifiers
 FH 1..312 "pro-region"
 Region
 FT 89..91 "/note- "N-glycosylation site."
 FT 313..316 "/note- "Proteolytic processing site"
 FT 317..436 "/note- "C-terminal mature domain"
 FT 352..382 "/note- "Consensus conserved motif (AMF95641)"
 FT XX
 PN WO9614335-A1.
 XX
 PD 17-MAY-1996.
 XX
 PF 07-NOV-1994; 94WO-US12814.
 XX
 PR 07-NOV-1994; 94WO-US12814.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Chang SC, Luyten FP, Moos M;
 XX
 DR WPI; 1996-251714/25.
 DR N-PSDB; AAT31662.

XX
 PT New purified cartilage extracts and proteins - used to stimulate the development and repair of cartilage in vivo.
 XX
 PS Claim 11; Fig 2; 34 pp; English.

XX
 CC The sequence represents cattle articular cartilage-derived morphogenetic protein-2 (CDMP-2). The N-terminal methionine and signal peptide is missing, but part of the pro-region, a typical proteolytic cleavage site and a C-terminal domain containing 7 highly conserved Cys residues characteristic of the transforming growth factor-beta gene family are present. A single N-glycosylation site is located in the pro-region. A consensus highly conserved motif in CDMP Proteins (AMF95641) is present in the C-terminal domain. CDMP-2 is present in a purified cartilage extract (claimed) which stimulates local cartilage formation and repair when combined with a matrix and implanted in a mammal. The protein may be used in therapy of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or to repair cartilage after reconstructive surgery.

Sequence 436 AA:

Qy 3 DLSHTPLRQKYLFDVMSLSDKEELVGAELLFRQAPSAPNGPAGPLHVLFCPLSPLL 62
 Db 112 dlshtplrkqylfdvmsldeelvgaellfrqapsapngpagsplhvlfcplsppl 196
 .Qy 3 DLSHTPLRQKYLFDVMSLSDKEELVGAELLFRQAPSAPNGPAGPLHVLFCPLSPLL 62
 Db 112 dlshtplrkqylfdvmsldeelvgaellfrqapsapngpagsplhvlfcplsppl 196
 .Qy 63 LDARTLDQPGAPPAGWENFDWQGLRHOPWKOLCLEDRAWGELDAGEEARARGQQPP 122
 Db 112 dlshtplrkqylfdvmsldeelvgaellfrqapsapngpagsplhvlfcplsppl 196
 .Qy 63 LDARTLDQPGAPPAGWENFDWQGLRHOPWKOLCLEDRAWGELDAGEEARARGQQPP 122
 Db 171 gsaep-gpgeaprgwefdwqglrhopwkolkledrawgeldageearargqqpp 229
 .Qy 122 PPPDLRLSGFGRRYRPPQERALLVFTRSQRNLFAEMREQLGSA-EAAGPGAGAGSW- 179
 Db 230 pppdlrlsgfgrryrrpperallvftrsqrnlfaemreqlgssatevgggaaegsgp 289
 .Qy 180 -----PPPSGAPDARWLPSGPGRERRRTAFASRHKRGKKSRERCSKKPLHVNFEKG 233
 Db 290 ppppppppsgtpdq1wspsg-rrrrtafasrhgkrgkkksrlcskpk1hvnfkely 348

Query Match 234 WDDWIIAIPLEYAYHCEGVCDPLRSHEPTNHAIOTLMNSMDPGSTPPSCCVPTKLTP 293
 DB 349 wddwiiapleyayhcegvcdplrsheptnhaiotlmnsmdpgstppsccvptkltp 408
 Query 294 ISLYVIDAGNNVYVKQYEDMYVEESGCR 321
 DB 409 islyidagnnvynveyemvesgcr 436

RESULT 6
 ID AAR78739 standard; Protein; 263 AA.
 XX
 AC AAR78739;
 XX DT 23-NOV-1995 (first entry)
 XX DF Murine mv2 protein..

Bone morphogenetic protein; mv2; tendon; ligament.
 ...
 OS Mus musculus.
 XX FH Key Location/Qualifiers
 FT Misc-difference 54
 FT /label= P,T
 XX PN WO0516035-A.
 XX PD 15-JUN-1995.
 XX PF 06-DEC-1994; 94WO-US14030.
 XX PR 02-NOV-1994; 94US-0333576.
 PR 07-DEC-1993; 94US-0164103.
 PR 25-MAR-1994; 94US-0217780.
 XX PA (GEMY) GENETICS INST INC.
 (HARD) HARVARD COLLEGE.
 XX PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
 PI Wozney JM;
 XX DR WPI: 1995-224320/29.
 DR N-PSDB; AAQ96224.
 XX Bone morphogenetic proteins -12 and -13 and corresp. DNA - used in
 compsn. for inducing tendon/ligament-like tissue formation
 ...
 PS Example: Page 71-72; 84pp; English.

XX Oligos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the
 CC amplification of a 269 bp DNA probe, the internal 269 bp of which
 CC corresponds to nt #607 to #865 of AAQ96207, from the BMP-12 encoding
 CC plasmid subclone PCRI-1#2. This probe was radioactively labelled
 CC and used to screen a murine genomic library. DNA sequence analysis
 CC of one of positively hybridising recombinants named MVR32 indicates
 CC that it encodes a portion of the mouse gene corresp. to the PCR
 CC product mv2 (murine homolog of the human VL-1 sequence AAQ96213).
 CC The partial DNA sequence of this subclone and corresp. AA
 CC translation are given in AAQ96224 & AAR78739.
 XX Sequence 263 AA:

Query Match 68.7%; Score 1207.5; DB 16; Length 263;
 Best Local Similarity 83.7%; Pred. No. 7.9e-100;
 Matches 231; Conservative 6; Mismatches 20; Indels 19; Gaps 4;
 Oy 46 PAGPLHVQFLPCLSPLLDARTLDPOGAPAGPAWEVDWQOLRHPWKQLCLELRAAWGE 105
 DB 7 pag-----ptirgssgtqpr---pag-ksfdwgqlrpqpkqclelraawge 51

Qy 106 LDAGEAEARARGPOOPPPDLSLGFFRRVPPORALLVVFTSRQTKNLFAEMREQLGS 165
 DB 52 1dxgatgararqgqppplars1gfrgrvrrpperalivflsqrknlfteqgs 111
 Qy 166 AEAAAGPGAGAEGSNWPPSGAPDAREPWLPSGRRRTAFASRHCKRKHSKRSRLRCSKKPL 225
 DB 112 aea---agaescpasgspdtgwlpssgrrrtfasringkrhokskrsrcsrip 167
 Qy 226 HVNFKELGWDWIIAPLEYAKCSCVCFPLSHLEPNHAITQTLANSMDPGSTPPSC 285
 DB 168 hvnftelgwdwiliapleyeayhcsgycdfplshleptnhaillqtlnmsmdpgstppsc 227
 Qy 286 CVPTRKTPISLYIDAGNNVYKQEDMVTESCCR 321
 DB 228 CVPTRKTPISLYIDAGNNVYKQEDMVTESCCR 263

RESULT 7
 ID AAW26595 standard; Protein; 263 AA.
 XX
 AC AAW26595;
 XX DT 21-JAN-1998 (first entry)
 DE Murine BMP-13 homologue fragment.
 XX KW BMP-13; bone morphogenetic protein; mouse; tendon; ligament;
 KW wound healing; tissue repair; carpal tunnel syndrome; tendonitis;
 KW therapy.
 XX OS Mus musculus.
 XX FH Key Location/Qualifiers
 FT Misc-difference 54
 FT /label= Pro, "Thr
 FT /note= "encoded by RCC"
 FT Misc-difference 247
 FT /note= "encoded by GTN"
 XX US5658882-A.
 XX PD 19-AUG-1997.
 XX PR 07-DEC-1993; 93US-0164103.
 PR 22-DEC-1994; 94US-0362670.
 PR 07-DEC-1993; 93US-0164103.
 PR 25-MAR-1994; 94US-0217780.
 PR 02-NOV-1994; 94US-0333576.
 XX PA (GEMY) GENETICS INST INC.
 (HARD) HARVARD COLLEGE.
 XX PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;
 PI Wozney JM;
 XX DR WPI: 1997-424270/39.
 DR N-PSDB; AA190397.
 XX PT Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52
 PT - useful for tissue healing and repair, treatment of tendonitis,
 PT improving fixation of tendons to bone etc
 XX Example 1; Column 69-72; 43pp; English.

This polypeptide comprises a fragment of a murine homologue of
 CC human bone morphogenetic protein 12 (BMP-12) (see also AAW6591).
 CC Its amino acid sequence was deduced from DNA subclone mV2 (see
 CC AAT90397), isolated from murine genomic DNA using primers (see
 CC AAT90393-94) based on human BMP-12 sequences. Human BMP-13, Bmp-12
 CC (see AAW26589) and M652 (see AAW26590) polypeptides are used in a

CC claimed method for inducing tendon and ligament formation.

XX Sequence 263 AA;

Query Match 68.7%; Score 1207.5; DB 18; Length 263;
Best Local Similarity 83.7%; Pred. No. 7.9e-100;
Matches 231; Conservative 6; Mismatches 20; Indels 19; Gaps 4;

Qy 46 PAGPLHVOLFCPSLPLDARLDPGAPPGWAEVWQGLRHPWKCLERAAWGE 105
DB 7 pag----ptlrsggtqr---pag-ksfdwqglrpwkqlcleraawge 51

Qy 106 LDAGEAEARARGPQQPPPDARSLSLGFGRRYRPQPQEFLALVVFTRSQRKNUFAEMREQLGS 165
DB 52 Ixdgdtararqqpppldrlsrglgrvpperalvvfrqrknitemheqgs 111

Qy 166 AEAAGPGAGAEGSWPPSGAPDARPLPSPGRRRTAFASRHRGKRSRLCSKKPL 225
DB 112 aea---aeaegscpapsgspatgspsgatpsgrrrrtfasrhgkrsrlcsrkpl 167

Qy 226 HVNFKELGWDWDTIAPLEYAETHCEGDFPLRSHEPEPTNAIQTLMNSMDPGSTPPSC 285
DB 168 hvnfkeliqwdwvdiapleyeyhcegvcdfplrsleptnahaiqtlmnsmdpgstppsc 227

Qy 286 CVPTEKLTPISLTYIDAGNNVYKYQEDMVYESCSCR 321
DB 228 CVPTEKLTPISLTYidagnnvkyqedmvyescscr 263

RESULT 8
AAE10985 standard; Protein: 263 AA.

AAE10985;

XX 18-DEC-2001 (first entry)

XX Murine partial mv2 protein.

XX Mouse; bone morphogenic protein; BMP-12; vulnerability; antiinflammatory; analgesic; gene therapy; transforming growth factor-beta; TGF-beta; tissue formation; wound healing; tissue repair; ligament defect; carpal tunnel syndrome; tendonitis; mv2.

OS Mus sp.

XX Key Location/Qualifiers
FH Misc-difference 54
FT /label= Unknown
FT /note= "Encoded by RCC"

-FT Misc-difference 247
FT /label= Unknown
FT /note= "Encoded by GTN"

XX US6284872-B1.

XX 04-SEP-2001.

XX 28-FEB-1997; 97US-0808324.

XX PR- 22-DEC-1994; 94US-0362670.

PR- 07-DEC-1993; 93US-0164103.

PR- 25-MAR-1994; 94US-0217780.

PR- 02-NOV-1994; 94US-0333576.

XX PA (GEMY) GENETICS INST INC.

(HARD) HARVARD COLLEGE.

XX Celeste AJ, Wozney JM, Rosen VA, Wolfman NM, Thomsen GH,

PI Melton DA;

XX DR WPI; 2001-588978/66.

N-PSDB; AAD18336.

XX New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects, comprises DNA encoding peptide linked to DNA encoding bone morphogenetic proteins (BMP)-12, BMP-13 or MP52 -

XX Example 1; Column 71-74; 42pp; English.

XX The invention relates to a chimeric DNA comprising a DNA sequence encoding a propeptide from a member of the transforming growth factor (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence encoding an amino acid sequence encoding a mature polypeptide consisting of Bone Morphogenic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA sequences are useful for producing proteins which induce tendon/ligament like tissue formation, and for isolating and cloning further DNA sequences encoding BMP-12 related proteins with similar activity. The proteins are useful for the induction of tendon/ligament-like tissue formation, wound healing, ligament and other tissue repair, augmenting the activity of bone morphogenetic proteins, and for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects. The present sequence is murine partial mv2 protein which is homologous to human BMP-12 or VL-1 sequences of the invention.

XX Sequence 263 AA;

SO Query Match 68.4%; Score 1202.5; DB 22; Length 263;

XX Best Local Similarity 83.3%; Pred. No. 2.2e-99; Matches 230; Conservative 6; Mismatches 21; Indels 19; Caps 4;

Qy 46 PAGPLHVOLFCPSLPLDARTLDPGQAPPAGWEVFDVWQGLRHPWKCLERAAWGE 105
DB 7 pag-----ptlsgsgtqr---pag-ksfdwqglrpwkqlcleraawge 51

Qy 106 LDAGEAEARARGPQQPPPDARSLSLGFGRRYRPQPQEFLALVVFTRSQRKNUFAEMREQLGS 165
DB 52 Ixdgdtararqqpppldrlsrglgrvpperalvvfrqrknitemheqgs 111

Qy 166 AEAAGPGAGAEGSWPPSGAPDARPLPSPGRRRTAFASRHRGKRSRLCSKKPL 225
DB 112 aea---aeaegscpapsgspatgspsgrrrrtfasrhgkrsrlcsrkpl 167

Qy 226 HVNFKELGWDWDTIAPLEYAETHCEGDFPLRSHEPEPTNAIQTLMNSMDPGSTPPSC 285
DB 168 hvnfkeliqwdwvdiapleyeyhcegvcdfplrsleptnahaiqtlmnsmdpgstppsc 227

Qy 286 CVPTEKLTPISLTYIDAGNNVYKYQEDMVYESCSCR 321
DB 228 CVPTEKLTPISLTYidagnnvkyqedmvyescscr 263

XX Query Match 68.4%; Score 1202.5; DB 22; Length 263;
XX Best Local Similarity 83.3%; Pred. No. 2.2e-99; Matches 230; Conservative 6; Mismatches 21; Indels 19; Caps 4;
XX Matches 230; Conservative 6; Mismatches 21; Indels 19; Caps 4;

Qy 46 PAGPLHVOLFCPSLPLDARTLDPGQAPPAGWEVFDVWQGLRHPWKCLERAAWGE 105
Db 7 pag-----ptlsgsgtqr---pag-ksfdwqglrpwkqlcleraawge 51

Qy 106 LDAGEAEARARGPQQPPPDARSLSLGFGRRYRPQPQEFLALVVFTRSQRKNUFAEMREQLGS 165
Db 52 Ixdgdtararqqpppldrlsrglgrvpperalvvfrqrknitemheqgs 111

Qy 166 AEAAGPGAGAEGSWPPSGAPDARPLPSPGRRRTAFASRHRGKRSRLCSKKPL 225
Db 112 aea---aeaegscpapsgspatgspsgrrrrtfasrhgkrsrlcsrkpl 167

Qy 226 HVNFKELGWDWDTIAPLEYAETHCEGDFPLRSHEPEPTNAIQTLMNSMDPGSTPPSC 285
Db 168 hvnfkeliqwdwvdiapleyeyhcegvcdfplrsleptnahaiqtlmnsmdpgstppsc 227

Qy 286 CVPTEKLTPISLTYIDAGNNVYKYQEDMVYESCSCR 321
Db 228 CVPTEKLTPISLTYidagnnvkyqedmvyescscr 263

XX RESULT 9
XX AAR40800
XX ID AAR40800 standard; Protein: 401 AA.
XX AC AAR40800;
XX DT 11-FEB-1994 (first entry)
XX DE TGF-beta like clone MP-52 protein.

XX Human; transforming growth factor; beta; TGF-beta; pharmaceutical; bone; cartilage; tooth; wound repair; immunosuppressor; organ transplant; cosmetic surgery; antibody; diagnosis
XX Homo sapiens.

XX PN WO9116099-A.

XX PD 19-AUG-1993.

XX PP 12-FEB-1993.

XX 93WO-EP00350.

XX PR 12-FEB-1992; 92EP-0102324.
 XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 XX PI Hoetten G, Neidhardt H;
 XX WPI; 1993-272824/34.
 DR N-PSDB; AAQ47709.
 XX PS Claim 11; Page 19; 29pp; English.
 XX CC The sequences given in AAR0800 and AAR5447 represent fragments of
 CC embryo and liver derived human transforming growth factor-beta
 CC (TGF-beta) respectively. The full length protein may be used in a
 pharmaceutical composition for the treatment of various bone, cartilage
 or tooth defects and in tissue and wound repair processes. These
 CC proteins may also be used as immunosuppressors in organ transplants and
 CC in cosmetic surgery. Antibodies raised against these proteins may be
 CC used for diagnostic purposes.
 XX SQ Sequence 401 AA;

Query Match 43.9%; Score 771; DB 14; Length 401;
 Best Local Similarity 51.1%; Pred. No. 1.3e-50;
 Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

Qy 9 LRRQKYLDFVSMIUSDKBELVGAELRLRFLRQAPS-----APWGPPAGPLHYQLFPCLS--- 59
 Db 117 vkrqyrfdisi-ekqiglgeirlirkpsdtakpaapggraqi- kisspsgrg 173
 Qy 60 -PLLDARTLDPOGAPPAGWEFDMQGLRH-QPAWKQLCLELRAAWGEAFAARG 117
 Db 174 pasldvrsv-pgldsgwefdiwlfrfnksaqicile-aw---ergra----- 221
 Qy 118 PQOPPPDPLRSIGFGRRVPPQERALLYVFTRSQRKNL-FAEMREOLGSAEAAGCAGAE 176
 Db 222 -----vdrlrgifdaraarghekaflvgirtkkrdfneikarsqddkt----- 268
 Qy 177 GSWPPPSGAPDARWLPSGPGRERRRTAFASHGKRHKGSPLRCSKKPLAVNFKELGWDD 236
 Db 269 -----yyeylfsg-q-zrkraplatzrqkpskmikarcrsrkahnfdmgwdd 316
 . 237 WIATPLEXEAYCEGYCDPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCCVPTKUTPISI 296
 Db 317 wiapleyeatfceicefpirsleptnavigtqimmsmdpestpptccvptrispis 376
 Qy 297 LYTDAGNNVVKYQXEDMAYVESGGCR 321
 Db 377 lfidsannvvkjqedmvivescgr 401

RESULT 10
 AAR69600 ID AAR69600 standard; Protein; 501 AA.
 XX AC AAR69600;
 XX DT 10-OCT-1995 (first entry)
 XX DE New TGF-beta family member MP-52 protein sequence.
 KW Transforming growth factor-beta family; mitogenic; differentiation;
 KW skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
 KW tissue regeneration; arthritis; ss.
 XX OS Homo sapiens.

XX XX Key FH FT FT Location/Qualifiers
 XX FT PN WO9504819-A.
 XX PD 16-FBB-1955.
 XX PF 09-AUG-1994; 94WO-EP02630.
 XX PR 10-AUG-1993; 93DE-4326629.
 PR 25-MAY-1994; 94DE-441822.
 PR 09-JUN-1994; 94DE-4420157.
 XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 XX PI Hotten G, Neidhardt H, Paulista M, Hoetten G;
 XX DR WPI; 1995-090897/12.
 DR N-PSDB; AAQ83695.
 XX PT New DNA encoding a new member of the TGF beta family - and
 PT related vectors, host cells etc., has mitogenic and
 PT differentiation inducing activity, e.g. for treating or
 PT preventing diseases of bone and cartilage etc.
 XX PS Claim 6; Page 36; 51PP; German.

Query Match 43.9%; Score 771; DB 16; Length 501;
 Best Local Similarity 51.1%; Pred. No. 1.7e-60;
 Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

Qy 9 LRRQKYLDFVMSLSDKEELVGAELRLRFLRQAPS-----APWGPPAGPLHYQLFPCLS--- 59
 Db 217 vrkqyrfdisi-kedglglaeirlirkpsdtakpaapggraqi-kisspsgrg 273
 Qy 60 -PLLDARTLDPOGAPPAGWEFDMQGLRH-QPAWKQLCLELRAAWGEAFAARG 117
 Db 274 pasldvrsv-pgldsgwefdiwlfrfnksaqicile-aw---ergra----- 321
 Qy 118 PQOPPPDPLRSIGFGRRVPPQERALLYVFTRSQRKNL-FAEMREOLGSAEAAGCAGAE 176
 Db 322 -----vdrlrgifdaraarghekaflvgirtkkrdfneikarsqddkt----- 368
 Qy 177 GSWPPPSGAPDARWLPSGPGRERRRTAFASHGKRHKGSPLRCSKKPLAVNFKELGWDD 236
 Db 369 -----yyeylfsg-q-zrkraplatzrqkpskmikarcrsrkahnfdmgwdd 416
 Qy 237 WIATPLEXEAYCEGYCDPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCCVPTKUTPISI 296
 Db 417 wiapleyeatfceicefpirsleptnavigtqimmsmdpestpptccvptrispis 476
 Qy 297 LYIDAGNNVVKYQXEDMAYVESGGCR 321
 Db 477 lfidsannvvkjqedmvivescgr 501
 RESULT 11
 AAW36100 ID AAW36100 standard; Protein; 501 AA.

Db	369	-----vyeysfsq--rrkratraqgkkrpsknilkarcerskahnfkdmqwd 416	Qy	118	PQQPPPPDLSLGFRRYRPOERALLVFTRSQRKNL-FAEMREOJGSABAAGPAGAE 176
Qy	237	WIAPILEYAYHCEGVCFPLRSHEPTNHAIOTLNMNSMDPCSTPPSCCVPTKLTPISI 296	Db	322	-----valrgigfdrarqvhckal.fivfgt.kkrdffneikarsqgddkt----- 368
Db	417	wiapleyeafhccegilecpfirsleptahavigtlnmmsmdpestppctcvptrlspis 476	Qy	177	GSMPPPSGAPDARPPWLPSPGRERRRTAFASRHGKRICKKSRLRCSSKKPLHNFKELGWDD 236
Qy	297	LYIDAGNNVVKYKOEDMVYESCGR 321	Db	369	-----vyeysfsq--rrkratraqgkrsknlkarcsskalhnfkdmqwd 416
Db	477	lfidannvvykqyedmvvrescgr 501	Qy	237	WIAPILEYAYHCEGVCDPLSHLEPTNHAIOTLNMNSMPGSTPSCCVPTKLTPISI 296
RESULT 1.3			Db	417	wiapleyeafhccegilecpfirsleptahavigtlnmmsmdpestppctcvptrlspis 476
AAW11900	ID	AAW11900 standard; protein; 501 AA.	Qy	297	LYDAGNNVVKYKOEDMVYESCGR 321
XX	AC	AAW11900;	Db	477	lfidannvvykqedmvvrescgr 501
XX	AC		RESULT 14		
DT	28-OCT-1997	(first entry)	AAW01799		
VV			ID	AAW01799 standard; protein; 501 AA.	
Human high mol. wt. protein MP52, a growth/differentiation factor.			XX		
Growth factor; differentiation; bone induction; osteoporosis; teeth; tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails; wound healing; regeneration; skeletal disorder; fracture; dimer. OS Homo sapiens.			AC	AAW01799;	
XX	PN	W09704095-A1.	XX		
XX	PD	06-FEB-1997.	PD	16-JAN-1997.	
XX	PF	24-JUL-1996;	PF	12-JUL-1995;	
XX	PR	24-JUL-1995;	PR	12-JUL-1995;	
XX	PR	95JUP-0218022.	PR	95DE-1025416.	
(FARH) HOECHST JAPAN LTD.	PA	96WO-JP02065.	XX		
(FARH) HOECHST PHARM & CHEM KK.	PA		PA	(BIO-P-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.	
XX	PI	Fujino Y., Kawai S., Kimura M., Matsumoto T., Takahashi M;	XX	XX	
XX	DR	WPI; 1997-13236/12.	PI	Bechtold R., Hoetten G., Paulista M., Pohl J., Unsicker K;	
N-PADB; AAT61412.	XX		XX	WPI; 1997-078343/08.	
High molecular weight human MP52 growth or differentiation factor - promotes bone induction, is useful for treatment and prevention of bone disease	PT		DR	N-PSDB; ANT55405.	
XX	PT		PT	Medicaments contg. protein MP52 - useful for treating neurological disorders	
AAW11900 is a high mol. wt. form of a human growth/differentiation factor MP52. MP52 promotes bone induction and is useful for plastic reconstructive surgery, cosmetic facial treatment, bone transplantation and tooth implantation. It is also useful for the treatment and prevention of disorders of bone formation, bone, cartilage, joint, tissue, skin, mucous membranes, nails or teeth; for wound treatment and tissue regeneration; and for the treatment of skeletal disorders and fractures.	XX		XX	Claim 2: Pages 12-14; 21pp; German.	
Claim 1: Page 12-16; 25pp; Japanese.	XX		PS	Best Local Similarity 51.1%; Pred. No. 1.7e-60; Mismatches 46; Indels 52; Gaps 12; Score 771; DB 18; Length 501;	
CC	CC	CC	CC	The present sequence is the human MP52 protein, which is described in WO 9316099 and 9504819 as a member of the human transforming growth factor beta superfamily. Active MP52 can be used in a medicament to treat and prevent nervous system diseases, and/or to treat neuropathological conditions caused by nervous system ageing.	
Sequence 501 AA;	SQ	Sequence 501 AA;	SQ	Query Match 43.9%; Score 771; DB 18; Length 501; Best Local Similarity 51.1%; Pred. No. 1.7e-60; Mismatches 46; Indels 52; Gaps 12;	
Best Local Similarity 51.1%; Pred. No. 1.7e-60; Mismatches 46; Indels 52; Gaps 12;	Qy	9 LRRQKYLEFDVMSLSDKEELVGAELRLFRQAPS-----APWGPAGPLHYOLFPLCS--- 59	Qy	9 LRRQKYLEFDVMSLSDKEELVGAELRLFRQAPS-----APWGPAGPLHYOLFPLCS--- 59	
Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;	Db	217 vkrkyvfaisal ekdgilgaerilrkpsdtakaaaggrraaql - kllscpsqr 273	Db	217 vkrkyvfaisal ekdgilgaerilrkpsdtakaaaggrraaql - kllscpsqr 273	
Qy	60 -PLILDARTLDQGAPPAGCMEVFDWQGLRH-QPMWKOLCLELRAAWGELDAEARARG 117	Qy	60 -PLILDARTLDQGAPPAGCMEVFDWQGLRH-QPMWKOLCLELRAANGELDAEARARG 117		
Db	274 pasildvsv--pgldgsqjewfdiwlfrfnksaqicle-aw--ergra----- 321	Db	274 pasildvsv--pgldgsqjewfdiwlfrfnksaqicle-aw--ergra----- 321		

Db 274 pas1ldvrs - pg1ldgsgwefvdiklfrrnkqnsqclele - aw---- - ergra----- 321
 Qy 118 PQQPPPPDLRSIGFGRVVRPPOERALIVVFTRSQRNL - FAEMLREOLGSAEAAGPGAGAE 175
 CC bone diseases caused by abnormal bone metabolism such as osteoporosis. It also accelerates the healing of bone fractures,
 CC and is useful for orthopaedic reconstruction, bone transplantation,
 CC and dental therapeutics because of its bone morphogenetic activity.
 CC It is also effective for preventing/treating cartilage, skin,
 CC connective tissue, mucous membrane, teeth and epithelial disorders.
 CC Recombinant Mp52 Arg can be produced in host (e.g. CHO) cells
 CC utilising an isolated DNA sequence (AAT59729) in plasmid pMSS99.
 XX

Db 322 -----vdrgqfdraarqvkeffkdfneikarsqgqdkt----- 368
 Qy 177 GSWPPSGAPDARWLSPGRSPRRRTAFASRHKGKKSRLRCSKKPLHVNFKELGWDD 236
 CC Sequence 501 AA;

Db 369 -----veyltsq-rrkrraplat:qk-fpsknikarscrs:rhvnfkdmwgdd 416
 Qy 237 WITAPLEVEAYHGEGYCFEPLSHLEPTNHAITQTLMNMSHDPGSTPPSCCVPTKLTPISI 296
 Db 417 wiatapleyafeafoeglecfirshleptnhavitqtlmnsmdepstppccvptlspisi 476
 Qy 297 LYIDAGNNVVKYKOEDKMYEVSGCR 321
 Db 477 ifidsannvvkyqyednnvescgr 501

RESULT 15

AAW12770 standard; Protein; 501 AA.

AC AAW12770;
 XX
 DT 11-MAY-1997 (first entry)
 XX Human bone morphogenic factor MP52 Arg.
 DE Bone morphogenic factor; MP52 Arg; bone; cartilage; skin;
 KW connective tissue; mucous membrane; epithelium; teeth;
 KW wound healing; pulmonary; tissue regeneration; osteoporosis;
 KW bone fracture; dental implant; osteoblast.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..27
 Peptide /label= "Sig-peptide"
 FT Cleavage-site 380..381
 FT /note= "sequencing suggests MP52 Arg is processed
 .FT proteolytically at Arg380-Arg381."
 Cleavage-site 381..382
 FT /note= "alternative cleavage site at Arg381-Ala382"
 Mat_protein 381..501
 FT /label= "Mat_protein
 .FT /note= "nature Mp52 Arg preferred for use in
 compns. of the invention"
 VX W09706254-A1.

PD 20-FEB-1997.
 XX 02-AUG-1996; 96WO-EP03427.
 XX 03-AUG-1995; 95EP-0112241.
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKLUNG.
 XX Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;
 XX DR WPI; 1997-154261/14.
 XX DR N-PSDB; AAT59729.

PT New human bone morphogenetic factor, MP52 Arg - used in the treatment
 XX of osteoporosis and bone fracture, and for promoting bone regrowth
 XX
 PS Claim 1; Page 12-15; 26pp; English.
 CC Novel human bone morphogenetic factor MP52 Arg (AAT59729) is a growth
 CC factor that induces formation of cartilage from undifferentiated
 CC mesenchymal cells and which stimulates the differentiation and
 CC maturation of osteoblasts. It is effective for treating/preventing

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OM protein - protein search, using sw model
Run on: October 3, 2002, 15:39:08 ; Search time 23.43 Seconds
(without alignments)
334.640 Million cell updates/sec

Title: US-09-945-182-26
Perfect score: 1757

Sequence: 1 NSDLSHTPLRQKYLFDVSM.....GNNVVYKQYEDMNVESGCR 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *

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6: /cggn2_6/ptodata/2/iaa/backfile1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1757	100.0	321	1	US-08-362-670B-26	Sequence 26, Appl
2	1757	100.0	321	3	US-08-376C-26	Sequence 26, Appl
3	1757	100.0	321	4	US-08-808-324-26	Sequence 26, Appl
4	1757	100.0	321	5	PCT-US94-14030A-26	Sequence 26, Appl
5	1202.5	68.4	263	1	US-08-362-670B-32	Sequence 32, Appl
6	1202.5	68.4	263	3	US-08-333-576C-32	Sequence 32, Appl
7	1202.5	68.4	263	4	US-08-808-324-32	Sequence 32, Appl
8	1202.5	68.4	263	5	PCT-US94-14030A-32	Sequence 32, Appl
9	771	43.9	401	3	US-08-289-222E-3	Sequence 3, Appl
10	771	43.9	401	4	US-09-054-526B-3	Sequence 3, Appl
11	765	43.9	501	2	US-08-288-508C-2	Sequence 2, Appl
12	765	43.5	388	1	US-08-362-670B-34	Sequence 34, Appl
13	765	43.5	388	3	US-08-333-576C-34	Sequence 34, Appl
14	765	43.5	388	4	US-08-324-34	Sequence 34, Appl
15	765	43.5	388	5	PCT-US94-14030A-34	Sequence 34, Appl
16	765	43.5	495	1	US-08-455-559-10	Sequence 10, Appl
17	765	43.5	495	4	US-08-145-060-10	Sequence 10, Appl
18	765	43.5	495	5	PCT-US94-00657-10	Sequence 10, Appl
19	731	41.6	134	1	US-08-581-529B-6	Sequence 6, Appl
20	731	41.6	134	3	US-09-097-616-6	Sequence 6, Appl
21	691.5	39.4	294	1	US-08-362-670B-2	Sequence 2, Appl
22	691.5	39.4	294	4	US-08-808-324-2	Sequence 2, Appl
23	691.5	39.4	294	5	PCT-US94-07762-6	Sequence 2, Appl
24	691.5	39.4	294	5	PCT-US94-14030A-28	Sequence 2, Appl
25	691.5	39.4	294	5	PCT-US94-14030A-2	Sequence 7, Appl
26	661	37.6	119	1	US-08-581-529B-7	Sequence 4, Appl
27	661	37.6	119	3	US-09-097-616-7	Sequence 4, Appl

RESULTS 1
US-08-362-670B-26
; Sequence 26, Application US/08362670B
; Patent No. 558882
; GENERAL INFORMATION
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Rooney, John
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wolfman, Neil
; APPLICANT: Thomson, Gerald H.
; APPLICANT: Melton, Douglas A.
; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,670B
; FILING DATE: December 22, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: 5202-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-362-670B-26
; Query Match Best Local Similarity Score 175%; DB 1; Length 321;
; Matches 321; Conservative 0; Mismatches 0; Indels 0;
; Gaps 0;
; Qy 1 NSDLHTPLRQKYLFDVSMLSKEELVGAELRLPROAPSAPWGPAGLJHVQLPCLSP 60

RESULT 2
US 08 333-576C-26
; Sequence 26, Application US/08333576C
; Patent No. 6027919

GENERAL INFORMATION:
 APPLICANT: Celeste, Anthony J.
 APPLICANT: Wozney, John
 APPLICANT: Rosen, Vicki A.
 APPLICANT: Wolfman, Neil
 APPLICANT: Thomsen, Gerald H.
 APPLICANT: Melton, Douglas A.

TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333-576C
 FILING DATE: NO 6027919ember 2, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 32,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 100.0%; Score 1757; DB 3; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.3e-147; Length 321;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 NSDLSTHTPLRKRQYFLDVMSLSDKEELVGAELRLRQAPSAPWGPPAGP.LHVQLFPCLSP 60
 Qy 61 LLDDARTLDPQGAPPAGWEVFDWQGLRHOPWKOLCLEURANGELDAEAEARGPQQ 120
 Db 61 LLDDARTLDPQGAPPAGWEVFDWQGLRHOPWKOLCLEURANGELDAEAEARGPQQ 120
 Qy 121 PPPDPLRSLGFGRRVRPQEALLVFTSRQNLNAEMREQLGSAEAAGPGAAEGSWP 180
 Db 121 PPPPLRSLGFGRRVRPQEALLVFTSRQNLNAEMREQLGSAEAAGPGAAEGSWP 180
 Qy 181 PPSGAPDARWLPSGPRRRRTAFASRIGKRRHGGKSRLRCSKPLHYNFKELGWDDWIA 240
 Db 181 PPSGAPDARWLPSGPRRRRTAFASRIGKRRHGGKSRLRCSKPLHYNFKELGWDDWIA 240
 Qy 241 PLEYAYHCEGVCDPFLRSLHEPTNHALIQTLMNSMDGSTPPSSCCVPTKLTPISILYID 300
 Db 241 PLEYAYHCEGVCDPFLRSLHEPTNHALIQTLMNSMDGSTPPSSCCVPTKLTPISILYID 300
 Qy 301 AGNNVYKQYEDMVYESCGR 321
 Db 301 AGNNVYKQYEDMVYESCGR 321

RESULT 3
US-08-808-324-26
; Sequence 26, Application US/08808324
; Patent No. 6284872

GENERAL INFORMATION:
 APPLICANT: Celeste, Anthony J.
 APPLICANT: Wozney, John
 APPLICANT: Rosen, Vicki A.
 APPLICANT: Wolfman, Neil
 APPLICANT: Thomsen, Gerald H.
 APPLICANT: Melton, Douglas A.

TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333-576C
 FILING DATE: NO 6027919ember 2, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 32,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 100.0%; Score 1757; DB 4; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.3e-147; Length 321;
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-808-324-26

7 PAG ----- PTLRGSSGTOPR -- PAG - KSFDWQGLRPOPWKOLCELERAANGE 51

Db 106 LDAGEAARARGPOOPPPDPLRSJGFGRRVPPDRLVTRSRQKLNLAEMREQJS 165

Qy 52 LDXGDTGARARGQQPQPLDRSLGFGVRVPPDRLVTRSRQKLNLAEMREQJS 111

Db 166 AEAGPGAAEGSNMPPSGAPDARWLPSGPGRRRRTAFASRGKRGKKSRLRCSPKL 225

Qy 112 AEA --- AGEGSCPAPSGSPDTGSWLSPGPGRRRRTAFASRGKRGKKSRLRCSPKL 167

Db 226 HVNFKELGNDWIAPLAYEAYHCEGVCDPLRSHEPTNHAIQTLMNSMDPGSTPPSC 283

Qy 168 HVNFKELGNDWIAPLAYEAYHCEGVCDPLRSHEPTNHAIQTLMNSMDPGSTPPSC 227

Db 286 CVPKLTPISILYDAGNNVVKYQEDMVYESCCCR 321

Qy 228 CVPKLTPISILYDAGNNVVKYQEDMVYESCCCR 263

Db 228 CVPKLTPISILYDAGNNVVKYQEDMVYESCCCR 263

RESULT 9

US-08-289-222E-3

; Sequence 3, Application US/08289222E

; Patent No. 6120760

; GENERAL INFORMATION:

; APPLICANT: HOTTEN, GERTRUD

; APPLICANT: NEIDHARDT, HELGE

; BECHTOLD, ROLF

; APPLICANT: POHL, JENS

; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIKAIKO, MARMELSTEIN, MURRAY & ORAM

; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,

; STREET: SUITE 330

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14030A

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/164,103

FILING DATE: 07-DEC-1993

APPLICATION NUMBER: US 08/217,780

FILING DATE: 25-MAR-1994

APPLICATION NUMBER: US 08/333,576

FILING DATE: 02-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lazar, Steven R.

REGISTRATION NUMBER: 32,618

REGISTRATION NUMBER: 5202D-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617 491-8260

TELEFAX: 617 876-5851

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: Linear

MOLECULE TYPE: protein

PCT/US94-14030A-32

Query Match 68 4%; Score 1202.5; DB 5; Length 263;

Best Local Similarity 83.3%; Pred. No. 9.3e-99; 6; Mismatches 21; Indels 19; Gaps 4;

Matches 230; Conservative 6;

46 PGLPHVQLPECLSPLLDARTLDPGAGPAGMVFQGLRHPQWQLCLERAANGE 105

Qy

MOLECULE TYPE: protein
 US-08-289-22E-3

Query Match 43.9%; Score 771; DB 3; Length 401;
 Best Local Similarity 51.1%; Pred. No. 1.9e-6;
 Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

Qy 9 LRRQKLYEDVSMISDEKEVLGABRLRERQAS----APMGPAGPLHVQLFPLS--- 59
 Db 117 VRQRQYFDISAL-EKDGLGAAELRLRKKSDTAKPAAQGGRAQL- KLSSCSPSGRQ 173

Qy 60 -PLLEDARTLDPGAGPAGWEYDVGRLRH-QPNKQCLCELRRAAWEAARARG 117
 Db 174 PASLDVRSV--FGLDGGWEVFIWLFRNFNSAQCLE-AW--ERGRA----- 221

Qy 118 PQQPPPPDLRSIYGGRVVRPQERALLVETRSQKRNL-FAEMREQLGSAEAAGPGAGAE 176
 Db 222 -----YDRLGLGFDRAQVHKAFLFEGTKEKIDLFFERIKARSQDDKT----- 268

Qy 177 GSNPPSGAPDARPWLPSPGRERRPRTAFASRGKKGKKSSNLRCSSKKPLHVNFKELGWDD 236
 Db 269 -----*VEYELFSQ-RERKRAPLATRGKRSKLNKARCSRKALHVNFKGWDD 316

Qy 237 WIATPLEYAHYGBGVCDPLSHLEPTNHALQTLMNSMDPGSTPSCCVPTKLTPISI 296
 Db 317 WIATPLEYAHYGBGVCDPLSHLEPTNHALQTLMNSMDPSTPCCVPTLSPISI 376

Qy 297 LYDAGNNVVVKOYEDMVYVESCCR 321
 Db 377 LFIDSANNVVVKOYEDMVYVESCCR 401

RESULT 10
 US-09-054-526B-3

Sequence 3, Application US/09054526B
 ; Patent No. 6197550
 ; GENERAL INFORMATION:
 ; APPLICANT: H TTEN, GERTRUD
 ; APPLICANT: NEIDHARDT, HELENE
 ; APPLICANT: BECHTOLD, ROLF
 ; APPLICANT: POHL, JENS
 ; TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
 ; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIKALDO, MARMELSTEIN, MURRAY & ORAM LLP
 ; STREET: SUITE 330
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-5701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/054,526B
 ; FILING DATE: 03-APR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/289,222
 ; FILING DATE: 12-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 44 23 190,3
 ; FILING DATE: 01-JUL-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EPO 92102324,8
 ; FILING DATE: 12-FEB-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/00350
 ; FILING DATE: 12-FEB-1993
 ; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
 ; NAME: KITTS, MONICA CHIN
 ; REGISTRATION NUMBER: 36,105
 ; REFERENCE/DOCKET NUMBER: P564-8005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202/638-5000
 ; TELEFAX: 202/638-4810
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 LENGTH: 401 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-054-526B-3

Query Match 43.9%; Score 771; DB 4; Length 401;
 Best Local Similarity 51.1%; Pred. No. 1.9e-6;
 Matches 166; Conservative 61; Mismatches 61; Indels 52; Gaps 12;

Qy 9 LRRQKLYEDVSMISDEKEVLGABRLRERQAS----APMGPAGPLHVQLFPLS--- 59
 Db 117 VRQRQYFDISAL-EKDGLGAAELRLRKKSDTAKPAAQGGRAQL- KLSSCSPSGRQ 173

Qy 60 -PLLEDARTLDPGAGPAGWEYDVGRLRH-QPNKQCLCELRRAAWEAARARG 117
 Db 174 PASLDVRSV--FGLDGGWEVFIWLFRNFNSAQCLE-AW--ERGRA----- 221

Qy 118 PQQPPPDLSIYSLGFGRVVRPQERALLVETRSQKRNL-FAEMREQLGSAEAAGPGAGAE 176
 Db 222 -----YDRLGLGFDRAQVHKAFLFEGTKEKIDLFFERIKARSQDDKT----- 268

Qy 177 GSNPPSGAPDARPWLPSPGRERRPRTAFASRGKKGKKSSNLRCSSKKPLHVNFKELGWDD 236
 Db 269 -----*VEYELFSQ-RERKRAPLATRGKRSKLNKARCSRKALHVNFKGWDD 316

Qy 237 WIATPLEYAHYGBGVCDPLSHLEPTNHALQTLMNSMDPGSTPSCCVPTKLTPISI 296
 Db 317 WIATPLEYAHYGBGVCDPLSHLEPTNHALQTLMNSMDPSTPCCVPTLSPISI 376

Qy 297 LYDAGNNVVVKOYEDMVYVESCCR 321
 Db 377 LFIDSANNVVVKOYEDMVYVESCCR 401

.RESULT 11
 US-08-288-508C-2

; Sequence 2, Application US/08288508C
 ; Patent No. 5594094
 ; GENERAL INFORMATION:
 ; APPLICANT: H TTEN, GERTRUD
 ; APPLICANT: NEIDHARDT, HELENE
 ; APPLICANT: PAULISTA, MICHAEL
 ; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
 ; TITLE OF INVENTION: THE TGF- FAMILY
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nikaldo, Marmelstein, Murray & Oram LLP
 ; STREET: 655 Fifteenth Street N.W. Suite 330
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-5701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/054,526B
 ; FILING DATE: 03-APR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/289,222
 ; FILING DATE: 12-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 44 23 190,3
 ; FILING DATE: 01-JUL-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EPO 92102324,8
 ; FILING DATE: 12-FEB-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/00350
 ; FILING DATE: 10-AUG-1994
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 43 26 829.3
 FILING DATE: 10-AUG-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: DE P 44 18 222.8
 FILING DATE: 25-MAY-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: DE P 44 20 157.5
 FILING DATE: 09-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: JAHNS, Kristina M.
 REGISTRATION NUMBER: P-41,092
 REFERENCE/DOCKET NUMBER: P564-4019
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)638-5000
 TELEFAX: (202)538-4810
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 501 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-2888-508C-2

Query Match 43.9%; Score: 771; DB 2; Length: 501;
 Best Local Similarity 51.1%; Pred. No. 2.5e-60;
 Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

Qy 9 LRRQKYLEFDMSLSDKEELVGAELRUFQPLHQLVOLFPLS--- 59
 Db 217 VRQRVYDVISAL-EKDGLGAEIRKPKDTAKAPEGGRAQQL-KLSSCPSGRQ 273

Qy 60 *PLLDARTLDPGAPPNGWEYDVGQLRH-QPKNQLCLELRANGELDGEAFAARAG 117
 Db 274 PASLDYRSV--PGLDGSGWEYDFINWLFNKNSAQCLLE-AN--ERGRA---- 321

Qy 118 PQQPPPDDIISLGEGRRVPPQERALLYFTTSQRKQL-FAEMREOLGSAAAGPCGAAE 176
 Db 342 -----VDIRGLGCFDRAQHVKEKALFLVFGTKKRQDIFTNEIKARGQDKT----- 368

Qy 177 GSMPPPSGAPDARPWLPSPGRRRRTAFASRHHKRHKKSRLRCSKRPHYNKELGWD 236
 Db 369 -----VIVYLFSQ-RKRRRAPLATRGKPKSNKLKARCSRKALKHNFKDGMWD 416

Qy 237 WIAPLEYAYHCEGVCDPLRSHLEPTNHAIOTLNMSMDGSTPPSCSYPTKLTPISI 296
 417 WIAPLEYAYHCEGLCCEPLRSHLEPTNHAVITQTLNMSMDPESTPPTCVCPTRLSPSI 476

297 LYDAGNNVYKQEDMVYESCCR 321

Db 477 LFDSANNVYKQEDMVYESCCR 501

RESULT 12
 US-08-362-670B-34
 ; Sequence 34, Application US/08362670B
 ; GENERAL INFORMATION:
 ; APPLICANT: Celeste, Anthony J.
 ; APPLICANT: Wozney, John
 ; APPLICANT: Rosen, Vicki A.
 ; APPLICANT: Wolfman, Neil L
 ; APPLICANT: Thomsen, Gerald H.
 ; APPLICANT: Melton, Douglas A.
 ; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENETICS INSTITUTE, INC.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA

ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentInRelease #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/362,670B
 FILING DATE: December 22, 1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 32,618
 REFERENCE/DOCKET NUMBER: 5202-D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-362-670B-34

Query Match 43.5%; Score: 765; DB 1; Length: 388;
 Best Local Similarity 51.2%; Pred. No. 6.3e-60;
 Matches 172; Conservative 36; Mismatches 78; Indels 50; Gaps 10;

Qy 12 QKYLFDYVSMLSDEKEELVGAELRULFQD-APSAPWNGPPAGPLHVQLFPC---LSPLLDAR 66
 Db 77 QSFLFDYSSLNDADEVGAELVRGRSPSBGPSWTSPLLLSTCPGAARAPPLYSR 136

Qy 67 TLDPQCAPPGWEPVWQGLRH---OPWKQLCLELAQWGLDAGEAFAARAGPQP 121
 Db 137 AAEP--LVGQRWEAFYADAMRRHREPREPAFLLLRVAQGPV-----P 180

Qy 122 PPPDLSSLGF---GRVRPPOBRLVVTFRSQRK-NLFEMREQ---LGSAEAAGPGAG 174
 Db 181 SPLAFLRLGFWMGGGSAABERAVLUVSSRTQRKESLFRTRAORALGAASEP--- 237

Qy 175 AEGSWPPSGAPDARPWLPSPGRRRRTAFASRHHKRHKKSRLRCSKRPHYNKELGWD 225
 Db 238 ----LPDPGTGTASPRAVIGRRRRTALGTRTAQSGGGAGRGRGRGSRCSRKPL 292

Qy 226 HVNFKELGWDWIIAILEYEAYHCEGVCDPLRSHLEPTNHAIOTLNMSMDPGSTPPSC 285
 Db 293 HVDFKELGWDWIIAIPDYEAYHCEGLCCEPLRSHLEPTNHAIOTLNMSMAPDAPASC 352

Qy 286 CVPTKLTPIISLYIDGNINVYKQEDMVYESCCR 321
 Db 353 CVPARLSPIISLYIDANNVVYKQEDMVYESCCR 388

RESULT 13
 US-08-333-576C-34
 ; Sequence 34, Application US/08333576C
 ; GENERAL INFORMATION:
 ; Patent No. 6,027919
 ; APPLICANT: Celeste, Anthony J.
 ; APPLICANT: Wozney, John
 ; APPLICANT: Rosen, Vicki A.
 ; APPLICANT: Wolfman, Neil L
 ; APPLICANT: Thomsen, Gerald H.
 ; APPLICANT: Melton, Douglas A.
 ; TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENETICS INSTITUTE, INC.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA

COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,576C
 FILING DATE: NO. 6027919ember 2, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 32,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 34 :
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-333-576C-34

Query Match 43.5%: Score 765; DB 3; Length 388;

Best Local Similarity 51.28; Pred. No. 6.3e-60;
Matches 172; Conservative 36; Mismatches 78; Indels 50; Gaps 10;

Qy 12 QKYLFDVMSLDKEELVGAELRLFQ-APSAPWGPAGPLHVQFLPC---LSPILLDAR 66
 Db 77 QSFLFDVSSNDADEVGAELVLRGSPSPPSLJLSTCPGAARPRLLYSR 136
 Qy 67 TLDPQAPPAGWEVEDWQGLRH---OPWKQCLLELAANGELDAGEEARARGPOQP 121
 Db 137 AAEP--LVGQRWEADVADMRRHREPRPRACFLLRAVAGV----P 180
 Qy 122 PPDPLRSLGF---GRVRPQQERALLVFTSRQK-NLFAMREQ---LGAEAAAGPAG 174
 .Db 181 SPLALRRLGGPGWGGSAANERAVLWSSRTQRKESLFRIRAQARAALASEP--- 237
 Qy 175 AEGSNPPSGAPDARPWLSPGPRRRRTAFASRH-----GKRHGKKSLRCSKKPL 225
 Db 238 ---LPDPTGTASPRAVIGGRERRRRTAOGSGGAQRGRGRRGRCSRPL 292
 Qy 226 HVNFKELGDDWILAPLEYEAYHCEGVCDPLRSHLEPTNHAIQTLLNSMDPGTPPSC 285
 .Db 293 HVDFKELGDDWILAPLDYEAYHCEGICDPLRSHLEPTNHAIQTLLNSMAPDAAPASC 352
 Qy 286 CVPKLTPISILYIDAGNNVYVKQYEDMVYVESCCCR 321
 Db 353 CVPARLSPISILYIDAANNVYVKQYEDMVYEACCR 388

RESULT 14

US-08-324-34

Sequence 34, Application US/08808324

GENERAL INFORMATION:

- APPLICANT: Celeste, Anthony J.

- APPLICANT: Wozney, John

- APPLICANT: Rosen, Vicki A.

- APPLICANT: Wolfman, Neil

- APPLICANT: Thomser, Gerald H.

TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENETICS INSTITUTE, INC.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,576C
 FILING DATE: NO. 6027919ember 2, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 32,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 34 :
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-324-34

Query Match 43.5%: Score 765; DB 4; Length 388;
 Best Local Similarity 51.28; Pred. No. 6.3e-60;
 Matches 172; Conservative 36; Mismatches 78; Indels 50; Gaps 10;

Qy 12 QKYLFDVMSLDKEELVGAELRLFQ-APSAPWGPAGPLHVQFLPC---LSPILLDAR 66
 Db 77 QSFLFDVSSNDADEVGAELVLRGSPSPPSLJLSTCPGAARPRLLYSR 136
 Qy 67 TLDPQAPPAGWEVEDWQGLRH---OPWKQCLLELAANGELDAGEEARARGPOQP 121
 Db 137 AAEP--LVGQRWEADVADMRRHREPRPRACFLLRAVAGV----P 180
 Qy 122 PPDPLRSLGF---GRVRPQQERALLVFTSRQK-NLFAMREQ---LGAEAAAGPAG 174
 .Db 181 SPLALRRLGGPGWGGSAANERAVLWSSRTQRKESLFRIRAQARAALASEP--- 237
 Qy 175 AEGSNPPSGAPDARPWLSPGPRRRRTAFASRH-----GKRHGKKSLRCSKKPL 225
 Db 238 ---LPDPTGTASPRAVIGGRERRRRTAOGSGGAQRGRGRRGRCSRPL 292
 Qy 226 HVNFKELGDDWILAPLEYEAYHCEGVCDPLRSHLEPTNHAIQTLLNSMDPGTPPSC 285
 .Db 293 HVDFKELGDDWILAPLDYEAYHCEGICDPLRSHLEPTNHAIQTLLNSMAPDAAPASC 352
 Qy 286 CVPKLTPISILYIDAGNNVYVKQYEDMVYVESCCCR 321
 Db 353 CVPARLSPISILYIDAANNVYVKQYEDMVYEACCR 388

RESULT 15

PCT-US94-14030A-34
 Sequence 34, Application PC/TUS9414030A
 GENERAL INFORMATION:
 - APPLICANT: GENETICS INSTITUTE, INC.
 - APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
 - TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 - NUMBER OF SEQUENCES: 35
 - CORRESPONDENCE ADDRESS:
 - ADDRESSEE: GENETICS INSTITUTE, INC.
 - STREET: 87 CambridgePark Drive
 - CITY: Cambridge
 - STATE: Massachusetts
 - COUNTRY: USA
 - ZIP: 02140
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14030A
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/164,103
 FILING DATE: 07-DEC-1993
 APPLICATION NUMBER: US 08/217,780
 FILING DATE: 25-MAR-1994
 APPLICATION NUMBER: US 08/333,576
 FILING DATE: 02-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REFERENCE/DOCKET NUMBER: 32,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498-8260
 TELEFAX: 617 876-8511
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 388 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-14030A-34

Query	Match	Score	DB	Length
Qy	1.2 QKLFDVMSLDSKEELVGAELRLFRO-APSAWPAGPAGPHVQLFPC--	43.5%	5	388;
Db	77 QSFEDVSSLNDADEVGAAELVLRVLRGSPESGPSWTSPPILLSTCPGAAARPLLYSR	51.28	60	
Qy	67 TLDPGQAPPAGMEVFDYWGQLRH---	36	50;	
Db	137 AAED-LVGQRNEAFDADAMRRHRRPRPRAFLLRAVAGPV-----	1.1	1	
Qy	122 PPPDLRSGF--GRRYRPPQERALLYFTRFSORK-NLFAEMREQ--	4.0	180	
Db	181 SPIALRRQFGMPGGGSSAABERAVIIVVSSPTQRESLFREIARAQAAALASEP--	1.1	1	
Qy	175 AEGSWPPSGAPPDRPILPSGRRRTAFASRH-----	1.1	225	
Db	238 -----LPDGTGTASPVAVIGRRRRRTALAGTRTAQGGGGAGRGHRGRSICSRKPL	1.1	1	
Qy	226 HYNFKELGWDWNTIAPLEYEAHCEGVCDFFPLRSHLEPTNHAIOTLMNSMDPGSTPPSC	1.1	285	
Db	293 HVDEKELGWDWNTIAPLEYAHCEGLCDFPLRSHLEPTNHAIOTLNSMAPDAPASC	1.1	1	
Qy	286 CVPYTKLTDISTLXIDAGNNVYVKOYEDMMVYESCGCR	1.1	321	
Db	353 CVPARLSPSILWIDAANNVYVKOYEDMMVYBACGR	1.1	388	

Search completed: October 3, 2002, 15:39:09
 Job time: 235 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 15:39:44 ; Search time 29.81 Seconds
(without alignments)
1034.709 Million cell updates/sec

Title: US-09-945-182-26

Perfect score: 1757

Sequence: 1 NSDLSTHTPLRQKYLFDVSM.....GNNVVKYQYESDMVYESCGCR 321

Scoring table: BL0SUMS2

Gpop 10.0 , Gapext 0.5

Searched:

283138 seqs, 96089334 residues

#1 number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR71;*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	77.9	436	2	BS5452
2	771	43.9	501	2	JC2347
3	765	43.5	495	2	S43294
4	762	43.4	501	2	A55452
5	691	39.3	125	2	S43295
6	549	31.2	151	2	S43296
7	426.5	24.3	398	2	JH0688
8	425.5	24.2	398	2	JH0687
9	418.5	23.8	405	2	I50608
10	406.5	23.1	408	2	BKHU4
11	405.5	23.1	452	2	I49542
12	405.5	23.1	461	2	S52408
13	401	22.8	393	2	S31073
14	401	22.8	420	2	I49541
15	396.5	22.6	454	1	BKHU5
16	396	22.5	408	2	S38343
17	395	22.5	394	2	S45355
18	391	22.3	408	2	JH0801
19	388.5	22.1	396	1	BKHU2
20	387	22.0	430	2	JQ1184
21	386	22.0	431	1	BKHU7
22	385.5	21.9	402	2	A5056
23	384	21.9	313	2	I51284
24	384	21.9	426	2	JH0690
25	379	21.6	400	2	A49147
26	378	21.5	408	2	S58791
27	377	21.5	401	2	JH0689
28	375	21.3	353	2	I50607
29	369	21.0	588	2	A26158

RESULTS

8

Score

Match

Length

DB

ID

Description

RESULT 1
B55452
cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)

C; Species: Bos primigenius taurus (cattle)

C; Date: 10-Feb-1995 #sequence_change 26-May-2000

C; Accession: B55452

R; Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; K

R; Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; K

R; Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; K

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R; Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; K

R; Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; K

Query Match 77.9%; Score 1368; DB 2; Length 436;

Best Local Similarity 81.7%; Pred. No. 2e-95; 9; Mismatches 268; Conserv. Matches 268;

Indels 12; Gaps 6;

QY 3 DLSTHTPLRQKYLFDVSMLSDKBELYGAEFLRFLQAPASAPWGPAGPLHVQLFPCLSPPLL 62

Db 112 DLSTHTPLRQKYLFDVSMLSDKBELYGAEFLRFLQAPASAPWGPAGPLHVQLFPCLSPPLL 62

QY 63 LDARTLDPOGAPPAGWEVFDWGLRHPWKQOLCILERLRAA-GELDAGEAEARARGPQQP 121

Db 171 GSAEP-GRAGAPRGWEVFDWGLRHPWKQOLCILERLRAA-GEGPAADEARTPGRQQP 229

QY 122 PPPDLRSLGFGRRVRPQORALLVVFTTSQRNLFAENREQLGSA-EAAGPAGABSSW- 179

Db 230 PPPDLRSLGFGRRVRPQORALLVVFTTSQRNLFAENREQLGSA-EAAGPAGABSSW- 179

QY 180 -----PPPSGAPDARPWLPSPGRRRTAFASRHGKRHGKSRSLRCSKKP-LHNPKELG 233

Db 290 PPPPPPSSGTPGAGLWPSG-RRRTAFASRHGKRHGKSRSLRCSKKP-LHNPKELG 348

QY 234 WDDM1IAPLEYAHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTP 293

Db 349 WDDM1IAPLEYAHCEGVCDPFLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTP 408

QY 294 ISILYIDAGNNVVYKYOYEVDMMVVESGCR 321

Db 409 ISILYIDAGNNVVYNEYEMVVESGCR 436

RESULT 2

JC2347

growth/differentiation factor 5 - human

C; Species: Homo sapiens (man)

C; Date: 20-Feb-1995 #sequence_change 17-Mar-2000

C;Accession: JC2347
R: Hoettien, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.
Biochem. Biophys. Res. Commun. 204, 646-652, 1994
A;Title: Cloning and expression of recombinant human growth/differentiation factor 5.
A;Reference number: JC2347; MUID:95071375
A;Accession: JC2347
A;Molecule type: DNA
A;Residues: 1-501 <stop>
A;Cross-references: GB:X80915; NID:9671524; PID:9671525
C;Genetics:
A;Gene: GDB:BMP9
A;Cross-references: GDB:433948
A;Introns: 211/1
C;Superfamily: inhibitin
C;Keywords: glycoprotein
F;189/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;381-382/Cleavage site: Arg-Ala (unidentified protease) #status predicted

Query Match 43.9%; Score 771; DB 2; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.6e-50;
Matches 166; Conservative 46; Indels 52; Gaps 12;

Db 9 LRRQKYLEDVSMSLSDKEELVGAELRLRFOAPS----APWGGPAGPVHQLVPLCLS--- 59
Db 217 VRKQRYVEDISAL-EKDGLGAEELRLKKPSDTAKAAPGGGRAAQL-KLSSCPGSRQ 273

Query Match 43.9%; Score 771; DB 2; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.6e-50;
Matches 166; Conservative 46; Indels 52; Gaps 12;

Db 60 -PLLDARTLDQPGQAPPAGPWEVFDWQGLRH-OPWKQLCLELRAANGELDAEEARARG 117
Db 274 PASLDDVRSV-PGLDGSWEVFDIWLKFERNFKNSAQCLLE AW--ERGA----- 321

Query Match 43.9%; Score 771; DB 2; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.6e-50;
Matches 166; Conservative 46; Indels 52; Gaps 12;

Db 118 PQQQPPDLSLGFGRYVRPQEORALLYVFTRSORKNL-FAEMREOLGSAEAAGPGGAE 176
Db 322 ----VDLRGLGFDRAAQHVKHEALKFLVGRKTKRDIFNEKARSQDDKT----- 368

Query Match 43.9%; Score 771; DB 2; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.6e-50;
Matches 166; Conservative 46; Indels 52; Gaps 12;

Db 177 GSWPPSGAPDARPWLPSPGRRRTAFASRHKGRGKSKSRLCSKKPLHVNFKEGLWD 236
Db 369 ----VYELFLSQ-RRKRPALATRQKRPSKNLKACCSRKAHLVNFKDMWD 416

Query Match 43.9%; Score 771; DB 2; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.6e-50;
Matches 166; Conservative 46; Indels 52; Gaps 12;

Db 237 WIAPLEYAHCCEGVCDPELRSHLEPTNHAIQTLMNSMDPSTPPSCCVPTKLTPISI 296
Db 417 WIAPLEYAHCCEGLCCEPPLSRSHLEPTNHAYIQTLMNSMDPSTPPCCVPTRLSPISI 476

Query Match 43.9%; Score 771; DB 2; Length 501;
Best Local Similarity 51.1%; Pred. No. 1.6e-50;
Matches 166; Conservative 46; Indels 52; Gaps 12;

Db 477 LFDSANNVYVQYEDMVYESCCR 501

RESULT 3

4.3294 One morphogenetic protein-related protein (GDF5) - mouse
C;Accession: S43294
R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A;Title: Limb alterations in brachyopodism mice due to mutations in a new member of the T
A;Reference number: S4294; MUID:94195427
A;Accession: S4294
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-495 <stop>
C;Superfamily: inhibitin

Query Match 43.5%; Score 765; DB 2; Length 495;
Best Local Similarity 50.5%; Pred. No. 4.5e-50;
Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

Db 9 LRRQKYLEDVSMSLSDKEELVGAELRLKKPSDTAKAAPGGRAAQL-KLSSCPGSRQ 238
Db 211 VRKQRYVEDISAL-EKDGLGAEELRLKKPSDTAKAAPPRSRRAAQLKLSSCPGSRQ 274

Query Match 43.5%; Score 765; DB 2; Length 495;
Best Local Similarity 50.5%; Pred. No. 4.5e-50;
Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

Db 61 LLIDARTLDQPGAPPAGPWEVFDWQGLRH-OPWKQLCLELRAANGELDAEEARARGP 119
Db 270 ALLDYRSV -PGLDGSWEVFDIWLKFERNFKNSAQCLLE AW--ERGA----- 315

Query Match 43.5%; Score 765; DB 2; Length 495;
Best Local Similarity 50.5%; Pred. No. 4.5e-50;
Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

Db 120 QPPPDPDLSLGFGRYVRPQEORALLYVFTRSORKNL-FAEMREOLGSAEAAGPGAGAE 178
Db 316 ---VDLRGLGFERTQVHEALKFLVGRKTKRDIFNEKARSQDDKT----- 362

Query Match 43.5%; Score 765; DB 2; Length 495;
Best Local Similarity 50.5%; Pred. No. 4.5e-50;
Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

Db 179 WPPPSGAPDARPWLPSPERRTAFASRHKGRGKSKSRLCSKKPLHVNFKEGLWD 238
Db 363 ----VYELFLSQ-RRKRPALATRQKRPSKNLKACCSRKAHLVNFKDMWD 412

Query Match 43.5%; Score 765; DB 2; Length 495;
Best Local Similarity 50.5%; Pred. No. 4.5e-50;
Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

Db 239 IAPLEYAHCCEGVCDPELRSHLEPTNHAIQTLMNSMDPSTPPSCCVPTKLTPISIY 298
Db 413 IAPLEYAHCCEGLCCEPPLSRSHLEPTNHAYIQTLMNSMDPSTPPCCVPTRLSPISI 472

Query Match 43.4%; Score 762; DB 2; Length 501;
Best Local Similarity 50.6%; Pred. No. 7.6e-50;
Matches 164; Conservative 46; Mismatches 64; Indels 50; Gaps 11;

Db 60 PLLDARTLDQPGAPPAGPWEVFDWQGLRH-OPWKQLCLELRAANGELDAEEARARGP 118
Db 275 ALLDYRSV -PGLDGSWEVFDIWLKFERNFKNSAQCLLE ----- 327

Query Match 43.4%; Score 762; DB 2; Length 501;
Best Local Similarity 50.6%; Pred. No. 7.6e-50;
Matches 164; Conservative 46; Mismatches 64; Indels 50; Gaps 11;

Db 9 LRRQKYLEDVSMSLSDKEELVGAELRLKKPS-DTAKAPPRSRRAAQLKLSSCPGSRQ 274
Db 217 VRKQRYVEDISAL-EKDGLGAEELRLKKPS-DTAKAPPRSRRAAQLKLSSCPGSRQ 274

Query Match 43.4%; Score 762; DB 2; Length 501;
Best Local Similarity 50.6%; Pred. No. 7.6e-50;
Matches 164; Conservative 46; Mismatches 64; Indels 50; Gaps 11;

Db 60 PLLDARTLDQPGAPPAGPWEVFDWQGLRH-OPWKQLCLELRAANGELDAEEARARGP 118
Db 275 ALLDYRSV -PGLDGSWEVFDIWLKFERNFKNSAQCLLE ----- 320

Query Match 43.4%; Score 762; DB 2; Length 501;
Best Local Similarity 50.6%; Pred. No. 7.6e-50;
Matches 164; Conservative 46; Mismatches 64; Indels 50; Gaps 11;

Db 119 QQPQPPDLSLGFGRYVRPQEORALLYVFTRSORKNL-FAEMREOLGSAEAAGPGAGAE 177
Db 321 ----VDLRGLGFERTQVHEALKFLVGRKTKRDIFNEKARSQDDKT----- 368

Query Match 43.4%; Score 762; DB 2; Length 501;
Best Local Similarity 50.6%; Pred. No. 7.6e-50;
Matches 164; Conservative 46; Mismatches 64; Indels 50; Gaps 11;

Db 178 SWPPPSGAPDARPWLPSPERRTAFASRHKGRGKSKSRLCSKKPLHVNFKEGLWD 237
Db 369 ----VYELFLSQ-RRKRPALATRQKRPSKNLKACCSRKAHLVNFKDMWD 417

Query Match 43.4%; Score 762; DB 2; Length 501;
Best Local Similarity 50.6%; Pred. No. 7.6e-50;
Matches 164; Conservative 46; Mismatches 64; Indels 50; Gaps 11;

Db 238 IAPLEYAHCCEGVCDPELRSHLEPTNHAIQTLMNSMDPSTPPSCCVPTKLTPISIY 297
Db 418 IAPLEYAHCCEGLCCEPPLSRSHLEPTNHAYIQTLMNSMDPSTPPCCVPTRLSPISI 477

Query Match 43.4%; Score 762; DB 2; Length 501;
Best Local Similarity 50.6%; Pred. No. 7.6e-50;
Matches 164; Conservative 46; Mismatches 64; Indels 50; Gaps 11;

Db 298 YIDAGNNVYVQYEDMVYESCCR 321
Db 478 FIDSANNVYVQYEDMVYESCCR 501

S43295 bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
 N;Alternate names: growth and differentiation factor 6
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
 C;Accession: S43295
 R;Storm, E.B.; Huyah, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
 Nature 368, 639-643, 1994
 A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
 A;Reference number: S43294; MUID:94195427
 A;Accession: S43295
 A;Molecule type: DNA
 A;Cross-references: EMBL:U08338; NID:9488463; PID:AAA18779.1; PID:9488464
 C;Genetics:
 A;Gene: Gdf6
 C;Superfamily: inhibin
 F;1-5/Domain: polypeptide recognition site #status predicted <PPR>
 F;6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted <N>

Query Match 39.3%; Score 691; DB 2; Length 125;
 Best Local Similarity 99.2%; Pred. No. 4.1e-45;
 Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 197 RRRRTAFAASRGRGERHGRKSRRLRSKPKLHVNFKEKGMDWDTIAPLEYAHCEGVCDFP 256
 Db 1 RRRRTAFAASRGRGERHGRKSRRLRSKPKLHVNFKEKGMDWDTIAPLEYAHCEGVCDFP 60
 Qy 257 LRSLEPTHTAIOTLMNSMDPSTTPSCCVPKLTPISILYDAGNNVVKQYEDMVVE 316
 Db 61 LRSLEPTHTAIOTLMNSMDPSTTPSCCVPKLTPISILYDAGNNVVKQYEDMVVE 120
 Qy 317 SGCCR 321
 Db 121 SGCCR 125

RESULT 6
 S43296 bone morphogenetic protein-related protein (GDF7) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
 C;Accession: S43296
 R;Storm, E.B.; Huyah, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
 Nature 368, 639-643, 1994
 A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
 A;Reference number: S43294; MUID:94195427
 C;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:U08339; NID:9488465; PID:AAA18780.1; PID:9488466
 C;Superfamily: inhibin

Query Match 31.2%; Score 549; DB 2; Length 151;
 Best Local Similarity 59.5%; Pred. No. 2.3e-34;
 Matches 103; Conservative 13; MisMatches 35; Indels 22; Gaps 1;
 Qy 149 RSQRKNLFAMREOLIGSAAAAGPGAGAEWSWPPSGAPDARPLPSGRRRTAFASRH 208
 Db 1 RRRRTAFAASRGRGERHGRKSRRLRSKPKLHVNFKEKGMDWDTIAPLEYAHCEGVCDFP 268
 Qy 209 GKRHGKSKPLHRSKPKLHVNFKEKGMDWDTIAPLEYAHCEGVCDFPRLSHLEPTNHA 268
 Db 39 GRHGGRGSRCSRSKSLHVDFKEGLWDMDTIAPILDYEAHCEGVCDPLRSHLEPTNHA 98
 Qy 269 IOTLMNSMDPSTPPSCCVPKLTPISILYDAGNNVVKQYEDMVVE 321
 Db 99 IOTLMNSMDPSTPPSCCVPKLTPISILYDAGNNVVKQYEDMVVE 151

RESULT 7
 JH0688 bone morphogenetic protein 2II precursor - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C;Accession: JH0688
 R;Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
 Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
 A;Title: Genes for bone morphogenetic proteins are differentially transcribed in ear;
 A;Reference number: JH0687; MUID:92378616
 A;Accession: JH0688
 A;Molecule type: mRNA
 A;Residues: 1-398 <NIS>
 A;Cross-references: GB:X63425; NID:964583; PID:CAA45019.1; PID:964584
 A;Experimental source: oocyte
 R;Plessow, S.; Koester, M.; Knochele, W.
 Biochem. Biophys. Acta 1089, 280-282, 1991
 A;Title: cDNA sequence of Xenopus laevis bone morphogenetic protein 2 (BMP-2).
 A;Reference number: S16244; MUID:91274367
 A;Accession: S16244
 A;Molecule type: mRNA
 A;Residues: 1-618, 'S', 8-15, 'V', 17-232, 'N', 234-398 <PLE>
 A;Cross-references: EMBL:X55031; NID:964581; PID:CAA38850.1; PID:964582

R;King, J.A.; Marker, P.C.; Seung, K.J.; Kingsley, D.M. Dev. Biol. 166, 112-122, 1994	Qy 121 PPPDPLSLGFGRVYRPPQERALLYVFTRSO-----RKNLFAEMREQLSAEAAAGP 171 Db 284 -PTDAGVVGVGN--NEGREFMVFQFRNEEVITNSHLRNRAOTRKKG-----332
A;Title: BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice A;Reference number: I49542; MUID:95046894	Qy 172 GAGAEGSWPPSGAPPDARPNIIFPSPGRRRR---TAFASRHKGKKSRLRCSSKKPLHV 227 Db 333 -----S-GRPRPDTNDIAS-DSASSLNSDQCARKNLV 367
A;Status: preliminary; translated from GB/EMBL/DDJB A;Molecule type: mRNA A;Residues: 1-452 <RES> A;Cross-references: GB:L41145; NID:9755033; PID:g755034	Qy 228 NFKEGLWDDWIIAPLEYEAYHCEGYODFPLRSHLFEPTNHAIIQTLMNSMDPGSTPPSCCV 287 Db 368 NFEDLWQENTIAPLGGVAFYCOGCGCAFPLNGHANTNHAIVOTLVHHHSPLSHYQPCCCA 427
C;Genetics: C;Gene: BMP5 C;Superfamily: inhibin	Qy 288 PTKLSPISILYIDAGNNVYVKQYEDMVXESGC 320 Db 428 PTKLSPITVYDDSRNVVLLKKYKNNMVRAGC 460
Query Match 23:18; Score 405.5; DB 2; Length 452; Best Local Similarity 29.0%; Pred. No. 4.2e-23; Matches 96; Conservative 54; Mismatches 126; Indels 55; Gaps 8;	RESULT 13 S37073 bone morphogenetic protein 2 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 *text_change 16-Jul-1999 C;Accession: S37073 R;Feng, J.Q.; Chen, D.; Peng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E. submitted to the EMBL Data Library, September 1993 A;Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogene A;Reference number: S37073 A;Accession: S37073 A;Molecule type: mRNA A;Residues: 1-593 <PEN> A;Cross-references: EMBL:Z225868; NID:g397950; PID:CAA81088.1; PID:g397951 C;Superfamily: inhibin
Qy 1 NSDLSHTPLRKQYLEDVSMLSDEKEBLVGELFLRFLRQAPAPGPPGPHVQFLPCLSP 60 Db 165 DKDFSHORRHYLKDFFDLTQPHGEAVTAEEFRYKDKGHNRHENET--IKISIYQIKE 222	Query Match 22:8%; Score 401; DB 2; Length 393; Best Local Similarity 30.8%; Pred. No. 7.9e-23; Matches 105; Conservative 50; Mismatches 98; Indels 88; Gaps
Qy 61 -----LLDARTLDPQGAPPAGMEFWYDQWLGRH---QPKWKLCELERAANGELDAG 109 Db 223 YTNRADLFLPDTRKQ--ALDVGVLWFDITVTSNHWVNPQNNLQLQCAETGD--G 276	Qy 2 SDSLHTPLRQKYLEFVSMLSDEKEBLVGELFLRFLRQAPAPGPPGPHVQFLPCLSPL 61 Db 120 SEMSGTSRR-EFFNLLSP-EPFLSSQAEQIFQMOFALGNSFOHRINTEBIKPA 177
Qy 110 EAEARARGPQQPPPDLRSLGFGRRVRPQERALLYVFTRSQRQSKNLFAEMREQLSAEAA 169 Db 277 RS-----INVKSAGLVRGHPQSKQPKMVAFFRASE---VLRSVRAASKR 320	Qy 62 -----LLDARTLDPQGAPPAGMEFWYDQWLGRH---QPKWKLCELERAANGELDAGEA 111 Db 178 TASSKFPVTRLDTRLYTN--ISQWESEFDVTPAWMR-W-----TAQGHTNNGFV 224
Qy 170 GPAGAEGSWPPSGAPPDARWLPSPGRRRTAFASTRHKGKKSRLCSKPKLHVNF 229 Db 321 NQNRNSKNSHQDPSRMPSA-----QDNYTSQKQACKKHELYVS 360	Qy 112 EARARGPOOPPPDLRSLGFGRRVRPQERALLYVFTRSQRKLNFAEMREQLSAEAA 171 Db 225 VEVAHIEKPV-----GYSKR-----HVRTRSLSHQD-----250
Qy 230 KELGDDWDDWIIAPLEYEAYHCEGYODFPLRSHLFEPTNHAIIQTLMNSMDPGSTPPSCCVPT 289 Db 361 RDGQWDWIIAPEGYAAYFCGECSFPPLNHNMAINTNHAIVOTLVHLMFPDHVPKPCAPT 420	Qy 172 GAGAEGSWPPSGAPPDARPNIIFPSPGRRRTAFASTRHKGKKSRLR-C 220 Db 251 ---EISW-----SOVRPLVTFGDKGHPLHREKRO-----KIKQRKRKSSC 293
Qy 290 KLTPIISILYIDAGNNVYVKQYEDMVXESGC 320 Db 421 KLNAAISVLFDDSSNVLKTYRNMYVRSGC 451	Qy 221 SKPLIVVNFKEGDWDWIIAPLEYEAYHCEGVCDPFLRSHLFEPTNHAIIQTLMNSMDPGS 280 Db 294 KRHPLYVDFSDVGWNWIVAPPGYHAFYCHGECPPFLADUNSTNHAIYOTLVNSV-SK 352
RESULT 12 S52408 SPDVRI protein - sea urchin (Strongylocentrotus purpuratus) C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 08-May-1995 #sequence revision 21-Jul-1995 #text_change 20-Sep-1999 A;Description: SpDVRI, a member of the transforming growth factor-beta superfamily expressed in sea urchin. Submitted to the EMBL Data Library, February 1995 A;Reference number: S52408 A;Accession: S52408 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-461 <PON> A;Cross-references: EMBL:Z48313; NID:g673496; PID:g673497 C;Superfamily: inhibin	Qy 281 TPPSCCVPTKLTPIISILYIDAGNNVYVKQYEDMVXESGC 321 Db 353 IPKACCVPTELSAISMLYLDENEKTVLKNYQDMVYEGCGR 393
Query Match 23:18; Score 405.5; DB 2; Length 461; Best Local Similarity 32.4%; Pred. No. 4.2e-23; Matches 108; Conservative 42; Mismatches 104; Indels 79; Gaps 12;	RESULT 14 I49541 bone morphogenetic protein 4 - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 *text_change 16-Jul-1999 C;Accession: I49541; S29533; B4201 R;Feng, J.Q.; Chen, D.; Cooney, A.J.; Tsai, S.Y.; Fer J. Biol. Chem. 270, 28364-28371, 1995 A;Title: The mouse bone morphogenetic protein-4 (BMP4) gene: Analysis of promm
Qy 13 KYLFDSVMSLSDKEELVGAELFLRQAPAPGPPGPHVOLF-----PCLSPILLDAR 66 Db 182 RYRFDIGRIPQGETVSAELRVFRDA--GRGRSLRYIDVLLRERGDSRSRSPYLD 239	Qy 67 TLDPOGQAPPAGMEFWY---WQGLRHPWKQCLCELERAANGELDAGAEARARGPOO 120 Db 240 IV-----GAGDHSWLVFEMTSATSTW--RSFGANVGLQVE-SIQLQNLID-----283

A; Reference number: I49541; MUID:96081880
 A; Accession: I49541
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-420 <RES>
 A; Cross-references: GB:L47400; PIDN: AAC37698_1; PID: q994734
 R; Dickinson, M.E.; van der Meer-de Jong, R.; Hogan, B.L.M.
 submitted to the EMBL Data Library, December 1990
 A; Description: Nucleotide sequence of the mouse Bone Morphogenetic Protein-4 (BMP-4) cDNA
 A; Accession number: S29523
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 13-420 <DCI>
 R; Dickinson, M.E.; Kobrin, M.S.; Silan, C.M.; Justice, M.J.; Miller, D.A.
 Peeland, N.G.; Jenkins, N.A.
 Genomics: Chromosomal localization of seven members of the murine TGF-beta superfamily subunit
 A; Reference number: A34201; MUID:90228366
 A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 253-420 <DI2>
 C; Genetics:
 A; Gene: BMP-4
 A; Introns: 11/1; 137/1
 C; Superfamily: inhibin
 C; Superfamily: inhibin

C; Genetics:
 A; Gene: GDB:BMP5
 A; Cross-references: GDB:127595; OMIM:112265
 A; Map position: pter-qter
 C; Superfamily: inhibin
 C; Keywords: bone; glycoprotein
 ; 1-17/Domain: signal sequence #status predicted <SIG>
 F; 18-316/Domain: propeptide #status predicted <PRO>
 F; 317-454/Product: bone morphogenetic protein 5 #status predicted <MAT>
 F; 211,327,345,395/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.6%; Score 396.5; DB 1; length 454;
 Best Local Similarity 28.8%; Pred. No. 2e-22;
 Matches 98; Conservative 51; Mismatches 118; Indels 73; Gaps 9;

Query 1 NSDLISHTPLRQRYLFDSMILSDKEELVGAELRLFQAPSPAWGPPAGPLHQLPCLSP 60
 Db 167 DKDFSHQRHRYKEFRFDLTQIPHGAEVTAAFRIYKDRSNRFENET - IKISIVQIKE 224

Query 61 -----LLDARTLDLDPQGAPPAGPAGNEVFDWQGLRH---OPWKOLCDELRAANGELDA 109
 Db 225 YTNRDADIFLLDTRKAQ --ALDGWNLVEDITVTSHWWTINPQNNNGLQLQAEITGD--G 278

Query 110 EAFAARARGPQQPPPDLSLGFGRVPPQERALLYVFTRSORKNLFAEMREQLGSAA 169
 Db 279 RS -----INVKSGAIVLGVRGPQSOPKMYAF-----FKASEVLRVSRAA 318

Query 170 GPCAGAEGSWPPSGADAPWLPSPQRRTAFASRH-----GRHGKKSRLRC 220
 Db 319 NK -----RKNQNRNKSSSHQDSSRMSSVGDYNTSEOKQAC 353

Query 221 SKRPLHNFKELGWDDWIIAPLEYEAYHCEGVCDFFPLRSHLEPTNHAIOTLMNSMDPGS 280
 Db 354 KKHELYYSFRDQGWDWIIAPPGYAAYFCGECSFPNAHMATNHAIVQLVHLMFPDH 413

Query 281 TPPSCCVPTKLTPISTILYDAGNNVVYKKOYEDMVYESCGC 320
 Db 414 VPKPCCAPTKLNAISVLYFDSSNVILKYYRMVYRSCGC 453

Search completed: October 3, 2002, 15:39:45
 Job time: 181 sec

Query 116 RGQQQPQPPDLSLGFGRVPPQERALLYVFTRSORKNLFAEMREQLGSAAAGPGAGA 175
 Db 231 -----SPAVLR--WTREKQPNGLAIEVTHLHQTRHGHVIRSLPQSGDWAA- 279

Query 176 EGSWPPPSGAPDAPWLPSPGR-----RRRPAFASRHRGKRSRILRCSKPKPLHV 228
 Db 280 -----QLRPLLTVFGHDGRGHTLTRRAKRSPRKHKPQRSKRNKNCRHSLYVD 328

Query 229 FKEGLWDWIIAPLEYEAYHCEGVCDFLPLRSHLEPTNHAIOTLMNSMDPGSTPPSCCV 288
 Db 329 FSDVGNNDWIVAPPQYQAFYCHGGCPFLADHLNSTNHAIVQTLVNSVN-SSSTPKACCV 387

Query 289 TKLTPSILYIDAGNNVVYKKOYEDMVYESCGC 321
 Db 388 TELSAISMLYLDFTKVVLKNYQEMVEGGCR 420

RESULT 15
 BMHUS
 bone morphogenetic protein 5 precursor - human
 C; Species: Homo sapiens (man)
 C; Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C; Accession: A39263
 R; Celeste, A.J.; Iannuzzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, J.; Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
 A; Title: Identification of transforming growth factor beta family members present in bone
 A; Reference number: A39263; MUID:91088608
 A; Accession: A39263
 A; Molecule type: mRNA
 A; Residues: 1-454 <CEL>
 A; Cross-references: GB:M60314; GB:M38693; NID:9339559; PID:AAA36736_1; PID:9339560

Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5	P43021	mus musculu	1
protein - protein search, using sw model		P48970	strongyloce	1
on: October 3, 2002, 15:45:59 ;	Search time 17.39 Seconds	P0wv56	mus musculu	1
	(without alignments)	P20722	mus musculu	1
	714.720 Million cell updates/sec	Q9uk05	homo sapien	1
title: US-09-945-182-26		Q26974	tribolium c	1
		P22004	homo sapien	1
		P35621	brachydanio .	1
		P34822	gallus gallus	1
		Q04906	rattus norve	1
		P27091	drosophila	1
		P55105	mus musculu	1

卷之三

Best Local Similarity 51.1%; Pred. No. 2.9e-49; Matches 166; Conservative 46; Mismatches 61; Indels 52; Gaps 12;

DR PRINTS; PRO00438; GFCKSKNOT.

DR PRODOM; PD000357; TGF-beta; 1.

DR SMART; SM00204; TGFbeta_1.

DR PROSITE; PS00250; TGF_beta_1.

KW SIGNAL; Growth factor; Cytokine; Glycoprotein; Polymorphism.

FT SIGNAL 1 27

FT PROPEP 28 375

FT CHAIN 376 495 GROWTH/DIFFERENTIATION FACTOR 5.

FT DISULFID 394 460 BY SIMILARITY.

FT DISULFID 423 452 BY SIMILARITY.

FT DISULFID 427 494 BY SIMILARITY.

FT DISULFID 459 459 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 98 98 S -> P.

SQ SEQUENCE 495 AA; 54885 MW; CD005DE48185D2E3 CRC64;

Query Match Score 765; DB 1; Length 495;

Best Local Similarity 50.5%; Pred. No. 7.9e-49;

Matches 163; Conservative 50; Mismatches 62; Indels 48; Gaps 12;

Qy 9 LRRQQKLFDVSMISDKEELVGAELRQAPQ---SAPWGPPAGPL-HYQLEPCLSL---P 60

DB 211 VRKQRYFDISAL-EDGGLGAELRLRKPKLVDVAPAVPSGRVIAQLKUSSCPGRQPA 269

Qy 61 LLLDDARTLDPGAGPAPPASWEVEDVWQGLRH_QPWVKQCLLELAANGELDGEAEARAGPQ 119

DB 270 ALDVPVY- -POLDGSGWEVEIWKLFRNNSAQCLLE-AN--ERCR----- 315

Qy 120 QPPPDPDLRSLGFGRRVRPPQRERLVFTRSQRNL-FAENREQLGSAEAAGPGAGAEGS 178

DB 316 ---VDIRJGLGFERTRQVHEKAFLVFGRIKKRDFLFFNEIKARSGQDDKT----- 362

Qy 179 WPPPSGAPDAREWLPSGPGRRRRTAFASRGKQRHGKSRSRLCSKPKLPHVNFKELGWDW 238

DB 363 -----VYELFLSQ- -RKRKRAPLNRQRGRPSNLKARCSRKALHVNFKDMGDWWI 412

Qy 239 IAPLEYAHCGVGCDPELRSHLEPTNHAIOTLMMSMDPSTPPCTCVTPRLSPISI 298

DB 413 IAPLEYAHFCRGVCDEPLRSHLEPTNHAIOTLMMSMDPSTPPCCVTPRLSPSILF 472

RESULT 4

GDF5_MOUSE 3

ID GDF5_MOUSE STANDARD PRT; 495 AA.

AC P43127;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Growth/differentiation factor 5 precursor (GDF-5).

GN GDF5 OR GDF-5 OR BP.

OS Mus musculus (Mouse).

OC Mammalia; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCB_ TaxID=1090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CD-1; TISSUE=Embryo;

RX MEDLINE=9419527; PubMed=8145850;

RA Storm E. E., Huynh T. V., Copeland N.G., Jenkins N.A., Kingsley D.M., Lee S.-J.; Limb alterations in brachypodism mice due to mutations in a new member of the TGF beta-superfamily. ";

Nature 368:639-643(1994).

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC -1- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.

CC -1- DISEASE: DEFECTS IN GDF5 ARE THE CAUSE OF BRACHYPODISM WHICH MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTITIES REQUIRES A LICENSE AGREEMENT (SEE [HTTP://WWW.ISB-SIB.CH/ANNOUNCE/](http://www.isb-sib.ch/announce/) OR SEND AN EMAIL TO LICENSE@ISB-SIB.CH).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC DR EMBL; U08337; AAA18778_1; -.

CC DR HSSP; P12643; 3BMP.

CC DR MGI; MGI:35688; Gdf5.

CC DR InterPro; IPR002400; GF_cysknot.

CC DR InterPro; IPR01839; TGF-beta.

CC DR InterPro; IPR00111; TGFb_N.

CC DR Pfam; PF00019; TGF-beta_1.

CC DR Pfam; PF00688; TGFb_propeptide; 1.

RN SEQUENCE FROM N.A.

RC SPAIN-BALB/C; TISSUE=Liver;

RC MEDLINE=94195427; PubMed=8145850;

RX Nature 368:639-643(1994).

RA Storm E. E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M., Lee S.-J.; Limb alterations in brachypodism mice due to mutations in a new member of the TGF beta superfamily. ";

RA RT "Limb alterations in brachypodism mice due to mutations in a new member of the TGF beta superfamily. ";

RA RT SEQUENCE FROM N.A.

RC SPAIN-BALB/C; TISSUE=Liver;

RC MEDLINE=94195427; PubMed=8145850;

RX Nature 368:639-643(1994).

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL: X55031; CAA38850_1; -.

CC EMBL: X16244; CAA45018_1; -.

CC PIR: JH0687; JH0687.

DR HES1; P1643; 3BMP.

DR InterPro; IPR01839; TGF-beta.

DR InterPro; IPR00111; TGFb_N.

PFam; PF0019; TGF-beta_1.

DR PFam; PF00588; TGFb_propeptide; 1.

DR Protein; PD000357; TGF-beta; 1.

DR SMART; SM00204; TGFb_1_BETA_1; 1.

DR PROSITE; PS00250; TGF_beta_1; 1.

KW SIGNAL; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.

... SIGNAL; 1 23 POTENTIAL.

PROTEP; 24 284 BONE MORPHOGENETIC PROTEIN 2-I.

CHAIN; 285 398 BY SIMILARITY.

FT DISULFID; 298 363 BY SIMILARITY.

FT DISULFID; 327 395 BY SIMILARITY.

FT DISULFID; 331 397 BY SIMILARITY.

FT DISULFID; 362 362 INTERCHAIN (BY SIMILARITY).

FT CARBHYD; 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBHYD; 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBHYD; 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT; 7 7 S > P (IN REF. 2).

FT CONFLICT; 16 16 V > L (IN REF. 2).

FT CONFLICT; 233 233 N > T (IN REF. 2).

FT CONFLICT; 398 AA; 45575 MW; 150AC6A47D2E15F CRC64;

SEQUENCE

Query Match 24.3%; Score 426.5; DB 1; Length 398; Best Local Similarity 31.5%; Pred No. 2, 8e-24; Matches 105; Conservative 51; Mismatches 88; Indels 89; Gaps 13;

QY 1.2 OKYLFDSMISDKKEFLVGAELRLFQQAAPSAPWGPPAGPIH-VOLFPCLSPL----- 61

Db 1.32 QRFENNISSPNEELVTSERLIREQYEPFESDSSKHLRNIYD1VKPAAAAASRGPV 191

Qy 62 LLDAARTLDQGAPAGAEWFDWQGL--- RHOPWKQCLLELAANGELDAGEAFARA 115

Db 1.92 RLLDTLHHN---ESKWEEFDTPTAIKAWTHQHNGHVEY---NNLD----- 236

... 1.16 RSPQQPPPDILRSLGFRGRVRP---POERALLYVFTSRQLNLFAEMREOLGSAEAAG 170

2.37 -RDKNVPKKHVR---ISRSLTDPDKNWPIRPLLVTFSHD----- 273

Qy 1.71 PGAGAESWPPSGAPDAREWLPSPGRRRRTAFASRHKKGKKSRLR---CSKKPLHVN 228

Db 2.74 KGHALH---KROKRQA-----RHQRKRKUSSCRHPLVVD 306

Qy 2.29 FRELGDWWIATPLEYEAYHCEGYCDEPRLSHPLEPTNHAIQTLMNSMDPGSTRPPSCCV 288

Db 3.07 PSDVGNDWIVAPPYHAFTCHGRCPEPLADHUNLNUSTNQTLVNSNT-NIPKACCP 365

Qy 2.89 TRUTPISILYIDAGUNVVKYQEDMVVECGCR 321

Db 3.66 TELSAISMLYLDENEKVKLKNYQDMVVECGCR 398

RESULT 7

BMP_XENLA STANDARD; PRT; 398 AA.

ID BMP_XENLA

AC P30884

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Bone morphogenetic protein 2-II precursor (BMP-2-II).

OS Xenopus laevis (African clawed frog).

Qy	230 KELGNDWIIAPLLEYAYHCEGVCDPLRSLEPTNHAIOTLMNSMDPGSTPPSCCVPT 289	Qy	121 PPPDPLRSLGFGGRVRVPPGERALLYVFTRSQ ----- -RKNLFAEMREQLGSAEAAGP 171
Db	361 RDGLQDQDWIIAPLPEGAFFCDGECSFPNAHMATNHAIVOTLHMFDPHVFKPCCAPT 420	Db	284 -- PTDAVGVGVN - NIGREPMPMVFFQRNEEVIAINTSHURRNRAATORKG ----- 332
Qy	290 KLTPIISLYDAGNNVVVKOYEDMVESSCGC 320	Qy	172 GAGAEGSNPPSGAPDARPLWPSPGRRRR --- TAFASRHKRKGKKSLRCSKPKLHY 227
Db	421 KLNATSVLVFDDSNVILKYYRNMYVRSGCG 451	Db	333 ----- -GKRKPKDIDIASR DSASSLNSWQCKRKLNLPV 367
RESULT 11	DVR1_STRPU	STANDARD;	PRT; 461 AA.
ID	DVR1_STRPU	STANDARD;	PRT; 461 AA.
AC	P48969;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	DVR-1 protein homolog precursor.		
GN	DVR1.		
OS	Strongylocentrotus purpuratus (Purple sea urchin).		
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Strongylocentrotidae; Strongylocentrotus.		
C	NCBI_TAXID=7668;		
JX	JX_1		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Ponce M.R., Michel J.L., Davidson E.H.;		
RL	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (PROBABLE).		
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.		
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EMBL	Z48313; CAA88306.1; -		
HSSP	P18075; 1BMP.		
DR	InterPro; IPR002400; GF_cystnot.		
DR	InterPro; IPR001839; TGF-beta.		
DR	InterPro; IPR001111; TGFb_N.		
DR	Pfam; PF000119; TGF_beta_1.		
DR	Pfam; PF00688; TGFb_propeptide; 1.		
PRINTS	PR00438; GPCYSKNOT.		
DR	ProDom; PD000357; TGF-beta; 1.		
DR	SMART; SM00204; TGFb; 1.		
DR	PROSITE; PS00250; TGF_BETA_1; 1.		
DR	Growth factor; Cytokine; Glycoprotein; Signal.		
PT	PROPEP	1 30	POTENTIAL.
PT	PROPEP	31 338	DVR-1 PROTEIN HOMOLOG.
FT	CHAIN	339 461	BY SIMILARITY.
FT	DISULFID	360 426	BY SIMILARITY.
FT	DISULFID	389 458	BY SIMILARITY.
FT	DISULFID	393 460	BY SIMILARITY.
FT	DISULFID	425 425	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	149 402	N-LINKED (GLCNAC, .,.) (POTENTIAL).
FT	CARBOHYD	51881 MW; 2573D54B625F7EF CRC64;	N-LINKED (GLCNAC, .,.) (POTENTIAL).
SQ	SEQUENCE	461 AA;	
Query Match		23.1%	Score 405.5; DB 1; Length 461;
Best Local Similarity		32.4%	Pre. No. 1..le-22;
Matches 108; Conservative		42;	Mismatches 104; Indels 79; Caps 12;
YQ	13 KYLDVSMIISDKBELVGAELRLFRQAPSAPGWPAGPLHYOLF----- -PCLSPULLDAR 66		
Db	182 YYRFDIGRIPQGGETVSAELRYRFLDA -GROGRSLYRIDVLLERGSDSRSPVYLDST 239		
Qy	67 TWDQGAPAGNPFYFDV-----WQGLRHQPKQLCLELRAAGELDAGEAEARGPQQ 120		
Db	240 IV --GAGDHGWLFDMTSATSTW--RSYSGANGLQLRVE--SLQGINID----- 283		

Query Match	23.08;	Score 403.5;	DB 1;	Length 395;		FT PROPEP 20	279	BONE MORPHOGENETIC PROTEIN 2.
Best Local Similarity	30.58;	Pred. No. 1.3e-22;				FT CHAIN 280	393	BY SIMILARITY.
Matches 100: Conservative	51;	Mismatches 98;	Indels 79;	Gaps 12;		FT DISULFID 293	358	BY SIMILARITY.
						FT DISULFID 322	392	BY SIMILARITY.
Qy	12 OKYLFDSLSDEKEELVGAELRFLRQAPSAPWGPPLH-VQLFPCLSL-----					FT DISULFID 326	392	BY SIMILARITY.
Db	129 RREFEFLTSIPPEEFITSAELQFREMOEAEGDGGFHRIINTYEIIKPATANSKFPA-----					FT CARBOHYD 357	135	INTERCHAIN (BY SIMILARITY).
Qy	62 -LIDARTLDPOGAPPAGWEFDVWQGLERHQPKWQLCLELAIRAWGELDAGGAEARQPOQ-----					FT CARBOHYD 133	133	N-LINKED (GLCNAC. . .) (POTENTIAL).
Db	189 RLDTDLVQN---TSWESFDTVTAVMR-W-----TAQGHANHGCFV-VEVTHLEE-----					FT CARBOHYD 161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).
Qy	121 PPPDPLRSLGFGGRVRP----POERALLYVETRSQRKNLFAEMREQLGSAEEAGPAGA-----					FT CARBOHYD 197	197	N-LINKED (GLCNAC. . .) (POTENTIAL).
Db	235 KOGVSKRHVRISLSLHDEHSUSQSIRELLTF-----					FT CARBOHYD 335	335	N-LINKED (GLCNAC. . .) (POTENTIAL).
Qy	176 EGSHPPPSGCAPDARWLPSGRRRRRTAFASRHKRKGKSRRL--CSKPKLHVNFNFKLG-----					SQ SEQUENCE 393 AA; 44383 MW; D2D20865652E0F213 CRC64;		
Db	269 D3RGEPHLH-----FREKQRA-----KHKQKRKLKSSCKRHPLYVDFSDVG-----							
Qy	234 WDDWIAFLPLEYEAYHCGSCVCDPLRSHLEPNHAIQTLMNSMDGOSTPSSCCVPTKLP-----							
Db	309 WNWIVAAPGYHAFYCHGCPPEPLADHLNSLNHAIQVTLVNSVN-SKIPRACCVPTELSA-----							
Qy	294 ISLYIDAGNNVYKYOEDMVYESCGCR 321							
Db	368 ISHLALDESEKVLKNYQDMVVEGCCR 395							
RESULT 13								
BMP2_RAT	ID	STANDARD;	PRT;	393 AA.				
AC	P95011;							
DT	01-FEB-1996 (Rel. 33, Created)							
DT	01-FEB-1996 (Rel. 33, Last sequence update)							
DT	16-OCT-2001 (Rel. 40, Last annotation update)							
DE	Bone morphogenetic protein 2 precursor (BMP-2)							
GN	BMP2 OR BMP-2							
OS	Rattus norvegicus (Rat)							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
MM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.							
NCBI_TAXID	10116;							
OX								
RN								
RP	SEQUENCE FROM N.A.							
RC	TISSUE-BONE;							
..	Feng J.-Q., Chen D., Feng M., Harris M.A., Mundy G.R., Harris S.E.;							
..	Submitted (Serp-1993) to the EMBL/GenBank/DBJ databases.							
..	-!- FUNCTION : INDUCES CARTILAGE AND BONE FORMATION.							
CC	-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.							
CC	-!- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.							
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.							
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CC	EMBL; Z23866; CAA81088.1; -.							
DR	HSSP, P12643; 3BMP.							
DR	InterPro; IPR01839; TGF-beta.							
DR	InterPro; IPR01111; TGFb_N.							
DR	Pfam; PF00019; TGF-beta; 1.							
DR	Pfam; PF00688; TGFb_propeptide; 1.							
DR	ProDom; PDO00357; TGF-beta; 1.							
DR	SMART; SMART004; TGFb_1.							
DR	PROSITE; PS00250; TGF_BETA_1; 1.							
KW	Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.							
FT	SIGNAL 1 19							
	POTENTIAL							

Clin. Orthop. Relat. Res. 294:344-352(1993).
 [4] SEQUENCE FROM N.A.
 STRAIN=129/SV; TISSUE=Liver;
 MEDLINE=96081880; PubMed=749338;
 PENG J.-P., Chen D., Cooney A.J., Tsai M., Harris M.A., Tsai S.Y.,
 Peng M., Mundy G.R., Harris S.E.;
 "The mouse bone morphogenetic protein-4 gene. Analysis of promoter
 utilization in fetal rat calvarial osteoblasts and regulation by
 COUP-TFI orphan receptor.";
 J. Biol. Chem. 270:28364-28373(1995).
 [5] SEQUENCE OF 241-408 FROM N.A.
 MEDLINE=90289866; PubMed=1970330;
 Dickinson M.E., Kobrin M.S., Silian C.M., Kingsley D.M., Justice M.J.,
 Miller D.A., Ceci J.D., Lock L.F., Lee A., Buchberg A.M.,
 Siracusa L.D., Lyons K.M., Deryck R., Hogan B.L.M., Copeland N.G.,
 Jenkins N.A.,
 "Chromosomal localization of seven members of the murine 'TGF-beta
 superfamily suggests close linkage to several morphogenetic mutant
 loci.";
 Genomics 6:505-520(1990).

CC -|- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION
CC -|- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC -|- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL; X56848; CAA40179.1; -.
 EMBL; S65032; AAB28021.1; -.
 EMBL; L47480; AAC37688.1; ALT_INIT.
 EMBL; D14814; BAA03555.1; -.
 PIR; B34201; B34201.
 PIR; S29523; S29523.
 HSSP; P12643; 3BMP.
 MGII; MGJ:8B180; Bmp4.
 InterPro; IPR001839; TGF-beta.
 InterPro; IPR001111; TGFb_N.
 Pfam; PF00019; TGF-beta; 1.
 Pfam; PF00658; TGFb_propeptide; 1.
 ProDom; PD000357; TGF-beta; 1.
 SMART; SM00244; TGFbeta; 1.
 PROSITE; PS000250; TGF-BETA1; 1.
 Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein

SIGNAL	1	19	POTENTIAL.
PROPEP	20	292	
CHAIN	293	408	BONE MORPHOGENETIC PROTEIN 4 .
DISULFID	308	373	BY SIMILARITY .
DISULFID	337	405	BY SIMILARITY .
DISULFID	341	407	BY SIMILARITY .
DISULFID	341	407	INTERCHAIN (BY SIMILARITY) .
DISULFID	372	372	N-LINKED (GLCNAC . . .) (POTENTIAL) .
CARBOHYD	144	144	N-LINKED (GLCNAC . . .) (POTENTIAL) .
CARBOHYD	209	209	N-LINKED (GLCNAC . . .) (POTENTIAL) .
CARBOHYD	350	350	N-LINKED (GLCNAC . . .) (POTENTIAL) .
CARBOHYD	365	365	N-LINKED (GLCNAC . . .) (POTENTIAL) .
CONFICT	407	407	C -> S (IN REF. 2).
CONFICT			

QY	564	PCLSPLLIDARTLDPOGAPPAGKVEFDVWQGLRHOPIKQLCLESRAWGELDAE EEAFA	115
Db	196	--LITRLDLTRLYHHN --VTRNETFDY-	218
Db	116	RGEQQPPPPDLSLGFGRVRPQPERRALLVVPTRSQRKNLPEAMREQLGSAE APAGA	175
Qy	219	--SPAVL --WTFRKPNYGLAIEVTIHLHQFRTHGOHVRSRSLPQGS DNA --	267
Qy	176	EGSWPPPSGAPDARPLWPSGR-----ERRTAPASRSHKRHGKKSRLRCS KPLHVN	228
Db	268	-----QLRPLLVTFGHDRGHTLRRRAKSPKHPQRSEKKNNCR SELVVD	316
Qy	229	PKELGWDDWIIAITLEAYHCYVCDFPLRSLEPTNHAIOTLMNSMDGST TCVP	288
Db	317	FSDYGWNDWIVAPPGYQFYCHGDCPPPLADHLNSTHATVQTLVNSVN-SS TCVP	375
Qy	289	TKTPISTLYIDAGNNVYYKQEDMIVESCGCR 321	
Db	376	TELSAISMLYLDDEYDKVVLNKYQEMVYEGCGER 408	
RESULT 15			
BMP4_RABBIT			
ID	0465776;	STANDARD;	409 AA.
AC	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Bone morphogenetic protein 4 precursor (BMP-4).		
GN	BMP4 OR BMP-4.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN			
RP	SEQUENCE FROM N.A. STRAIN IN NEW ZEALAND WHITE; TISSUE=Ocular ciliary epithelium;		
RC	Wan X.L., Sears J., Chen S., Sears M.;		
RA	"Cloning and expression of BMP-2/-4 from rabbit ocular ciliary epithelium.",		
RT	Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.		
RL	CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).		
CC	CC -!- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.		
CC	CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.		
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CC	DR AF042497; AAB97467.1; -.		
DR	HSSP_P12643; 3BMP.		
DR	InterPro; IPR01839; TGF-beta.		
DR	InterPro; IPR01111; TGF _b .N.		
DR	Pfam; PF000119; TGF-beta; 1.		
DR	PF00688; TGF _b _propeptide; 1.		
DR	ProDom; PD000357; TGF _b beta; 1.		
DR	SMART; SM00204; TGF _b ; 1.		
DR	PROSITE; PS000250; TGF_BETA; 1.		
KW	Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.		
FT	SIGNAL 1 19 POTENTIAL.		
FT	PROPEP 20 293 BY SIMILARITY.		
FT	CHAIN 294 409 BONE MORPHOGENETIC PROTEIN 4.		
FT	DISULFID 309 374 BY SIMILARITY.		
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FT	DISULF		

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FT CARBOHYD    209      209      N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD    351      351      N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD    366      366      N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE    409 AA: 46541 MW: 35557561447AD625 CRC64:
Query Match      22.7%; Score 398.5; DB 1; Length 409;
Best Local Similarity 31.4%; Pred. No. 3.2e-22; Gaps 10;
Matches 105; Conservative 42; Mismatches 98; Indels 89;
Qy 13 KYLEDVSLSDKEBLVGAELRER----QAPSAPWG-----PPAG -PLHVQLF 55
Db 140 REFLNLSSIPENEAISSEMLRLFREQVDQGPDWEGFHRMINIYEMKPPAEEAVPGH--- 195
Qy 56 PCLSPLLIDARTLDPOGAPPAGLWFDWQSLRHQPKQLCLELRAAWGELDAEARA 115
Db 196 --LITRLIDDTRLVHHN-- -VTRWETEDY----- 218
Qy 116 RGPOQQPPPDLSLGFGRVRVPPQERALVVYFTRSORKNLFAEMREOLGSAAAGPGAGA 175
Qy 219 -----SPAVLR--WTREKOPNHLGLAVEVTHFHTRTHQGQHVRLSRSLIQGSCDWA-- 267
Qy 176 EGSMAPPSPGADARPWLSPGR-----RRRTTAFASRIGKRIGKKSRURCSKKPLHV 227
Db 268 -----QFRPLLVTFGDGRHALTRRRAKRSLKHPQRARKNNCRHALIV 316
Qy 228 NFKELGMDWIIAPLEYAYHCEGYCDEPLSHLEPTNHA1TOTLMNSMDPGSTPPSCCV 287
Db 317 DFSDVGNNDWIVAPPGTOAFYCHGDCPFLADHFNSTNHA1VQTLLVNSVN-SSIPRACCV 375
Qy 288 PTKLTPISILYIDAGNNVYROYEDMVYESCCCR 321
Db 376 PTESLALSMLYLDNEYDKVVLKNYQEMVYEGGCCR 409

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Search completed: October 3, 2002, 15:46:00
Job time: 406 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 15:45:36 : Search time 48.58 Seconds
(without alignments)
1143.091 Million cell updates/sec

Title: US-09-945-182-26
Perfect score: 1757
Sequence: 1 NSDLSHTPRLRRQKYLFDVSM.....GNVVYKQYEDMVVESCCGR 321

Scoring table: BL2USM62
Gapext 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

:al number of bits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMPL_19:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp Rodent:
 12: sp_virus:
 13: sp_vertebrate:
 14: spUnclassified:
 15: sp_rvirius:
 16: sp_bacteriopl:
 17: sp_archeap:

ALIGNMENTS

RESULT	1	Q9W753	PRELIMINARY;	PRT;	399 AA.
ID	Q9W753;				
AC	Q9W753;				
DT	01-NOV-1999 (TREMBLrel. 12, Created)				
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 12, Last annotation update)				
DE	GROWTH AND DIFFERENTIATION FACTOR 6.				
GN	GDF6.				
OS	Xenopus laevis (African clawed frog)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batracia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopus.				
OC	Xenopodinae; Xenopus.				
OX	NCBI_TaxID=3555;				
[1]					
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=99396700; PubMed=10393114;				
RX	Chang C., Hemmati-Brivanlou A.;				
RA	"Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";				
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.				
DR	Development 126:347-357(1997).				
RT	RT 126:347-357(1997).				
DR	EMBL: AF155125; AAD38402.1; -				
DR	InterPro: IPR002405; Inhibin-alpha.				
DR	HSSP: P12643; 3BAP.				
DR	InterPro: IPR001839; TGF-beta.				
DR	InterPro: IPR01111; TGFb_N.				
DR	PIBM: PF000119; TGF-beta; 1.				
DR	PFAM: PF00668; TGFb_propeptide; 1.				
DR	PRINTS: PR00669; INHIBINA.				
DR	PRODOM: PD000357; TGF-beta; 1.				
DR	SMART: SM00204; TGFb; 1.				
DR	PROSITE: PS0250; TGF_BETA; 1.				
KW	Glycoprotein.				
SQ	SEQUENCE 399 AA; 45571 MW;	C549D973B50B8517 CRC64;			

Prev. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1000.5	56.9	399	13 Q9W753	Q9W753 xenopus lae
2	907	51.6	412	13 O12938	O12938 brachydanio
3	796	45.3	447	6 Q9BDW8	Q9BDW8 cercopithec
4	782	44.5	413	13 Q9DGN4	Q9DGN4 xenopus lae
5	771	43.9	501	4 Q96SB1	Q96SB1 homo sapien
6	756	43.0	500	13 Q9WWGO	Q946GO gallus galli
7	737	41.9	294	6 Q9BDW9	Q9BDW9 macaca fasc
8	712	40.5	324	13 Q9YH9	Q9YH9 gallus galli
9	698.5	39.8	261	13 Q9W6C0	Q9W6C0 brachydanio
10	664.5	37.8	257	13 Q42303	Q42303 brachydanio
11	634	36.1	441	11 Q99MY1	Q99MY1 mus musculu
12	612.5	34.9	126	13 Q93573	Q93573 gallus galli
13	451	25.7	277	13 Q90YB2	Q90YB2 lampetra ja
14	427.5	24.3	417	5 Q9XQ7	Q9XQ7 lytechinus
15	426	24.2	289	5 Q9XYQ8	Q9XYQ8 strongyloce
16	423.5	24.1	398	13 Q90YD7	Q90YD7 xenopus tro

Query Match 56.9%; Score 1000.5%; DB 13; Length 399;
Best Local Similarity 63.9%; Pred. No. 2.; e-79;
Matches 205; Conservative 29; Mismatches 54; Indels 33; Gaps 5;

Qy	3 DLSTPLRQKYLFDVMSLSDKEELVGAELRLRQAPSAPWGGPAGPLHVOLFPCLSLPLL 62	Db	118 DHNSPLWRQKYLFDVSLSENEVILGAELRVTKISGSFRASERGPVIEQASCOSHIV 177
Db	110 NSLSLSLRKRYLFDVSLSDKEELVGAELRLRQAPSAPWGGPAGPLHVOLFPCLSLPLL 169	Qy	63 LDARTLDPGAPPAGWEDYQKQGLR - HOPWKOLCLESRAANGELDAEAEARARGPQ 118
Qy	63 LDARTLDPGAPPAGWEDYQKQGLR - HOPWKOLCLESRAANGELDAEAEARARGPQ 120	Db	178 LDSQTLDLEDAHKPKWEVFDWEIWERQHSHGNFCLERAT --LONPPEI---- 229
Db	170 LDYRTLDRDTPSPGWQVEDVWSLSDISQSKQICVELKAI - SLITG - ----- 216	Qy	119 QQQPPPDLSIYGFGRRVRPQERALLYVFTRS-QRKNLFAEMREQLSAEEAEG 177
Qy	121 PPPDLRSLGGRVYRPOERAKLVFTSRQKNLFAEMREQLSAEEAAGPAGAESWP 180	Db	230 -----K 270
Db	217 -LEVNLRLSGLARKPRSHOEKAALLVVFTKSSRNLYNLEKEQHSSK----- 262	Qy	178 SWPPPGCAPDARPWLPSPGRRRRTAFASHRGKRICKKSRLRCSKPKLAVNFELGMDWW 237
Qy	181 PPSGADDARPWLSPGRRRRTAFASHRGKRICKKSRLRCSKPKLAVNFELGMDWW 240	Db	271 LMGLDTIGKERS - HSCTRTRALPVGKRGKKSRSRCSKPKLAVNFELGMDWW 328
Db	263 --SMKEAR - LHEKTRRARRRTTFNSRQKSRURCSKPKLAVNFELGMDWW 318	Qy	238 YIAPLEYAYHAEGVCDPLASHLEPTINHAIIQTLMNSMDGSTPESCCVPTMTPSIL 297
Qy	241 PLEYEAYHCEGVCDPLRSHLPEFTNHAIIQTLMNSMDGSTPESCCVPTMTPSIL 300	Db	329 YIAPLDXEAVHCEGMCDPLRSHLPEFTNHAIIQTLMNSMDGSTPESCCVPTMTPSIL 388
Db	319 PLEYEAHHEGVCDPLRSHLPEFTNHAIIQTLMNSMDGSTPESCCVPTMTPSIL 378	Qy	298 YIDAGNNVVVKOYEDMVESEGGCR 321
y	301 AGNNVVVKOYEDMVESEGGCR 321	Db	389 YIDAGNNVVVKOYEDMVESEGGCR 412
Db	379 AGNNVVVKOYEDMVESEGGCR 399		
RESULT			
		Q9BDW8	PRELIMINARY;
		ID	Q9BDW8
		AC	Q9BDW8;
		DT	01-JUN-2001 (TREMBLrel. 17, Created)
		DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
		DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
		DE	GROWTH/DIFFERENTIATION FACTOR 7.
		GN	GDF7.
		OS	Cercopithecus aethiops (Green monkey) (Grivet).
		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
		OC	NCBI_TAXID:9534;
		RN	[1]
		RP	SEQUENCE FROM N.A.
		RX	Medline#-21136583; PubMed#-11238730;
		RA	Watakabe A.; Fujita H.; Hayashi M.; Yamamori T.;
		RT	"Growth/differentiation factor 7 is preferentially expressed in the primary motor area of the monkey neocortex.";
		RT	J. Neurochem. 76:1455-1464 (2001).
		CC	- - SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
		DR	EMBL: AF254569; AAK30842.1; -
		DR	HSSP: P12643; AF254568; AAK30842.1; JOINED.
		DR	InterPro: IPR00839; TGF-beta.
		DR	InterPro: IPR01111; TGF _b N.
		DR	Pfam: PF00019; TGF-beta_1.
		DR	PFAM: PF00688; TGFB_propeptide; 1.
		DR	ProDom: PD000357; TGF-beta; 1.
		DR	SMART: SM00204; TGFB; 1.
		DR	PROSITE: PS00250; TGF_BETA; 1.
		KW	Glycoprotein.
		SQ	SEQUENCE 447 AA; 46866 MW; DF46D591925A89391 CRC64;
Query Match			
		Best Local Similarity	45.3%; Score 796; DB 6;
		Matches	Length 447;
		177	Conservative 52.8%; Pred. No. 2.1e-61;
			Mismatches 77; Indels 50; Gaps 10;
Qy	12 QKYLDPGAPPGEWYDWMQGLR-----OPWKQCLERLAANGELDAEAEARQGPQ 121	Db	136 QSFLEDVSSLNDADEVVGAEVLVRGSPESGPQSSTSPPLLSITCPGAAPELYSR 195
		Qy	67 TLDPGQAPPGEWYDWMQGLR-----OPWKQCLERLAANGELDAEAEARQGPQ 121
		Db	196 AAEP - LYGGRWEYDVADAMRRURREPRAFCUILLRATGCPVRS ----- 240
Qy	122 PPPDLRSLGIF - GRRVRVPQERALLYVFTRSQK - NLFAEMREQ -- LGSAEAEPCAG 174		
		3 DLSTPLRQKYLFDVMSLSDKEELVGAELRLRQAPSAPWGGPAGPLHVOLFPCLSLPLL 62	

DR PRINTS; PRO0669; INHIBINA.	DR SMART; SM00204; TGF-beta; 1.
DR PRODom; PD00037; TGF-beta; 1.	DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFbeta; 1.	KW Glycoprotein.
DR GLYCOPROTEIN.	FT NON-TER
FT NON-TER	1
FT NON-TER	324 AA; 324 MW; 0B8A7CB11375007 CRC64;
SQ SEQUENCE	29414 MW; 77346E977036A104 CRC64;
Query Match 9	Score 39.8%; Score 698.5%; DB 13; Length 261;
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 153; Conservatve 28; Mismatches 56; Indels 45; Gaps 9;	Matches 153; Conservatve 28; Mismatches 56; Indels 45; Gaps 9;
Query Match 60	PLLDAPT---LDPQGAPPAGNEFVDYQGLRHPHQK-----LCLELRAAWGELD 107
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;	Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;
Query Match 108	AGDAEARARGPOOPPPDRLRSQGFRVRPPOERALLYVPTRSORK_NLFAMPREOLGSA_166
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;	Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;
Query Match 58	VSDSNNEAVHPGM-----LGSLRDOOATHERALLYVAFSGARRENLFIREKIRAM 109
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;	Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;
Query Match 167	EAAGPGAGAEWSWPPSGAPDARPWLPSPGRRRTAFASR-----HGRHRHGKRSRLR 219
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;	Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;
Query Match 110	KS-----PKFSNPTPIPERISIKHP---RHRRRRTPLLAGPVGPTISGCKGGGRRT 159
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;	Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;
Query Match 220	CSSKKPLAHNFKEGLMDMIDIAPLEYEAYHCCEVYCDPFLPLRSLEPTNHAIOTLMNSMDPG 279
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;	Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;
Query Match 160	CSRKPLAHNFKEGLMDWIIAPLDEAYHCCEGLCDPFLPLRSLEPTNHAIOTLMNSMDPE 219
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;	Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;
Query Match 280	STPPSCCVPTKLPISILYIDAGNNWVYKQTEDAVYESCGR 321
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;	Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;
Query Match 220	STPPSCCVPSKLSPISILYIDSGNNWVYKQTEDMVYESCGR 261
Best Local Similarity 54.3%; Prod. No. 3 6e-53;	Best Local Similarity 54.3%; Prod. No. 3 6e-53;
Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;	Matches 151; Conservatve 46; Mismatches 67; Indels 50; Gaps 10;
RESULT 10	RESULT 10
ID 042303	PRELIMINARY;
AC 042303;	PRT; 257 AA.
DT 01-JAN-1998	(TREMBREL. 05, Created)
DT 01-JAN-1998	(TREMBREL. 05, Last sequence update)
DT 01-DEC-2001	(TREMBREL. 19, Last annotation update)
DE CONTACT	(FRAGMENT).
GN GDF5.	CONTACT (FRAGMENT).
OS Brachydanio rerio (zebrafish) (zebra danio).	OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.
NCB_TAXID=7955;	NCB_TAXID=7955;
RN [1]	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RX MEDLINE-97398455; PubMed=9256353;	RX MEDLINE-97398455; PubMed=9256353;
RA Bruneau S., Mourrain P., Rosa F.M.;	RA Bruneau S., Mourrain P., Rosa F.M.;
OC "Expression of contact, a new zebrafish DVR member, marks mesenchymal cell linesages in the developing pectoral fins and head and is regulated by retinoic acid.";	OC "Expression of contact, a new zebrafish DVR member, marks mesenchymal cell linesages in the developing pectoral fins and head and is regulated by retinoic acid.";
RL Mech Dev. 65:163-173(1997)	RL Mech Dev. 65:163-173(1997)
DR EMBL; Y12005; CAA:2733..1; -	DR EMBL; Y12005; CAA:2733..1; -
DR HSSP; P12643; 3BMP.	DR HSSP; P12643; 3BMP.
RA Poerlner D., Celeste A.J., Crosier K.E., Crosier P.S.;	RA Poerlner D., Celeste A.J., Crosier K.E., Crosier P.S.;
RT Isolation of zebrafish gdf7 and comparative genetic mapping of genes belonging to the Growth/Differentiation factor 5, 6, 7 subgroup of the	RT Isolation of zebrafish gdf7 and comparative genetic mapping of genes belonging to the Growth/Differentiation factor 5, 6, 7 subgroup of the
DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).	DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
DR InterPro: IPR001839; TGF-beta; 1.	DR InterPro: IPR001839; TGF-beta; 1.
DR Pfam: PF00119; TGF-beta; 1.	DR Pfam: PF00119; TGF-beta; 1.
DR PRINTS; PR00038; GFCSNNOT.	DR PRINTS; PR00038; GFCSNNOT.
DR PRODom; PD000357; TGF-beta; 1.	DR PRODom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.	DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.	DR PROSITE; PS00250; TGF_BETA; 1.
DR GLYCOPROTEIN.	DR GLYCOPROTEIN.
FT CHAIN 140	FT CHAIN 140
SQ SEQUENCE 257 AA;	SQ SEQUENCE 257 AA;
Query Match 37.8%; Score 664.5%; DB 13; Length 257;	Query Match 37.8%; Score 664.5%; DB 13; Length 257;
Best Local Similarity 51.8%; Pred. No. 3.e-50;	Best Local Similarity 51.8%; Pred. No. 3.e-50;

Matches	144;	Conservative	32;	Mismatches	53;	Indels	49;	Gaps	9;
Qy	52	VQLFPCLS---	PULLDARTLDPGQAPPAGNEVFDW-	-QGLRHQPKWQKLCLELRAANG	104			Qy	112
Db	21	LRFITCAGKNAVLLGARPPEDPSA -	SYWEVDIWKVKFNRNTP -	-QCLCLEDAA	73			Db	236
Qy	105	ELDAGEEARANGPQQPPPDLSRSLGFGRRVRPQERALLYVFRSQRKNLF -	AEMREQL	163				-PLAURRGCGWPGCGDGGTAAEVRTRTQKESLFRIRQAR	285
Db	74	-VHGR-----	-PLDLRLGLSLSRAGRTQEKAFFVFGRTKKRGLFYNEIKAR -	119				Qy	165
Qy	164	GSAEAAAGPAGAEGSNPPPSAPDARPLWPSPGRERRTAFASRKGKKSRLRCRSK	K 223					SAEAGPGAGAEWSWPPGAPDARPLWPS - PGRRRRTAFASRH	208
Db	120	-----	-SDHDNKTVYELFTQRMRRAPLPR - GKKPKPNPQRNCNK	159				Db	286
Qy	224	PLHVNFKELGNDWIIAPLEYEAHYCEGVQCDPLRSHELEPTNHAIQTLNMNSMDPGSTPP	283					- ALRAA ---AE - -PPDPGPAGSKRNALGRRRKTALAGTRGAOSGGGGGGGG	337
Db	160	QHVNFKELGNDWIIAPLEYEAHFQCDPLFPIRSHLEPTNHAIQTLNMNSMDPGSTPP	219					Qy	209
Qy	284	SCCVPTKLTPISLYIDAGNNVVKOYEDAVYVESGCR	321					- -GKRHKGSRSRCSKPKLHYNFKELGNDWIIAPLEYEAHYCEGVCDPPL	257
Db	220	TCCVPTRLSPISLYIDSANNVVKOYEDAVYVESGCR	257					Db	338
RESULT 11									
Q99MY1		PRELIMINARY;		PRT;	441 AA.			Qy	258
AC	Q99MY1;							RSHELEPTNHAIQTLNMNSMDPGSTPPSCCPYKLPISLYIDA 301	
DT	01-JUN-2001	(TREMBLrel.	17,	Created)				Db	398
DT	01-JUN-2001	(TREMBLrel.	17,	Last sequence update)				RSHELEPTNHAIQTLNMNSMDPGSTPPSCCPYKLPISLYIDA 441	
DT	01-DEC-2001	(TREMBLrel.	19,	Last annotation update)					
DE									
GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).									
GN									
OS									
Mus musculus (Mouse)									
OC									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxId=10096;									
OX									
RN	[1]								
RP									
SEQUENCE FROM N.A.									
STRAIN-TT2;									
RX									
Medline=21136583; Pubmed=11228730;									
Watake A., Fujita H., Hayashi M., Yamamoto T.; "Growth/differentiation factor 7 is preferentially expressed in the primary motor area of the monkey neocortex."; J. Neurochem. 76:1455-1464 (2001).									
-! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.									
DR	AF254571; AAC0843.1;								
EMBL;	AF254570; AAC0843.1; JOINED.								
DR	HSSP; P12643; 3BMP.								
DR	InterPro; IPR002405; Inhibin_alpha.								
DR	InterPro; IPR001839; TGF-beta.								
DR	InterPro; IPR001111; TGFbeta_N.								
DR	Pfam; PF00688; TGF-beta; 1.								
DR	PRINTS; PRO0665; INHIBINA.								
DR	ProDom; PD000357; TGF_beta; 1.								
DR	SMART; SM00204; TGFbeta_1.								
DR	PROSITE; PS00250; TGF_BETA; 1.								
KW	GLycoprotein.								
FT	NON_TER	1							
SQ	SEQUENCE 126 AA:	14265 MW:	CBB24D280F44A394 CRC64;						
Query Match	34.9%;								
Best Local Similarity	86.5%;								
Matches	109;	Conservative	30;	Mismatches	10;	Indels	6;	Gaps	1;
Qy	197	RRRRTAFASHRGK-HGKKSRLCRSKPLHVNFKELGNDWIIAPLEYEAHYCEGVCDF	255						
Db	1	RKRRRTIAASGGRHHKAKTRCSRKPVNFKELGNDWIIAPLDTEAYHCEGVCDF	60						
Qy	256	PLRSHEPTNHAIQTLNMNSMDPGSTPPSCCPYKLPISLYIDAGNWVYKQYEDMVV	315						
Db	61	PLRSHEPTNHAIQTLNMNSMDPETPPSCCVPSKLSPISLYIDSGNWVYKQYEDMVV	120						
Qy	316	ESCGCR 321							
Db	121	ETCGCR 126							
Matches	144;	Conservative	32;	Mismatches	53;	Indels	49;	Gaps	9;
Qy	52	VQLFPCLS---	PULLDARTLDPGQAPPAGNEVFDW-	-QGLRHQPKWQKLCLELRAANG	104			Qy	112
Db	21	LRFITCAGKNAVLLGARPPEDPSA -	SYWEVDIWKVKFNRNTP -	-QCLCLEDAA	73			Db	236
Qy	105	ELDAGEEARANGPQQPPPDLSRSLGFGRRVRPQERALLYVFRSQRKNLF -	AEMREQL	163				Qy	165
Db	74	-VHGR-----	-PLDLRLGLSLSRAGRTQEKAFFVFGRTKKRGLFYNEIKAR -	119				Db	286
Qy	164	GSAEAAAGPAGAEGSNPPPSAPDARPLWPSPGRERRTAFASRKGKKSRLRCRSK	K 223					Db	286
Db	120	-----	-SDHDNKTVYELFTQRMRRAPLPR - GKKPKPNPQRNCNK	159				Qy	209
Qy	224	PLHVNFKELGNDWIIAPLEYEAHYCEGVQCDPLRSHELEPTNHAIQTLNMNSMDPGSTPP	283					Db	338
Db	160	QHVNFKELGNDWIIAPLEYEAHFQCDPLFPIRSHLEPTNHAIQTLNMNSMDPGSTPP	219					Qy	258
Qy	284	SCCVPTKLTPISLYIDAGNNVVKOYEDAVYVESGCR	321					Db	398
Db	220	TCCVPTRLSPISLYIDSANNVVKOYEDAVYVESGCR	257					Qy	258
RESULT 12									
Q93573		PRELIMINARY;		PRT;	126 AA.				
AC	Q93573;								
DT	01-NOV-1998	(TREMBLrel.	08,	Created)					
DT	01-NOV-1998	(TREMBLrel.	08,	Last sequence update)					
DE									
GDF6/7.									
GN									
OS									
Gallicus gallus (Chicken)									
OC									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.									
NCBI_TaxID=9031;									
OX									
RN	[1]								
RP									
SEQUENCE FROM N.A.									
RN									
SEQUENCE FROM N.A.									
STRAIN-TT2;									
RX									
Medline=21136583; Pubmed=11228730;									
Watake A., Fujita H., Hayashi M., Yamamoto T.; "Growth/differentiation factor 7 is preferentially expressed in the primary motor area of the monkey neocortex."; J. Neurochem. 76:1455-1464 (2001).									
-! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.									
DR	AF254571; AAC0843.1;								
EMBL;	AF254570; AAC0843.1; JOINED.								
DR	HSSP; P12643; 3BMP.								
DR	InterPro; IPR002405; Inhibin_alpha.								
DR	InterPro; IPR001839; TGF-beta.								
DR	InterPro; IPR001111; TGFbeta_N.								
DR	Pfam; PF00688; TGF-beta; 1.								
DR	PRINTS; PRO0665; INHIBINA.								
DR	ProDom; PD000357; TGF_beta; 1.								
DR	SMART; SM00204; TGFbeta_1.								
DR	PROSITE; PS00250; TGF_BETA; 1.								
DR	GLycoprotein.								
FT	NON_TER	1							
SQ	SEQUENCE 441 AA:	441 MW;	74DA312A853701F0 CRC64;						
Query Match	36.1%;								
Best Local Similarity	44.5%;								
Matches	153;	Conservative	33;	Mismatches	70;	Indels	88;	Gaps	13;
Qy	12	QKYLFDVMSLSDKELYGAEELRLFQAPSAP-----	-----WGPYPAGPLHYLFP	56					
Db	132	QSFLEDVSSLSEAEVVAELRLRSPPEPDRDSATLLPRLLSTCPDEAGTAH	-----	186					
Qy	57	CLSPLLDARTLDQPGAPPAGNEVFDWQGLR_HQPV-----	-KQLCDELRLRAWGEJDAGEA	111					
Db	187	----LLHSRAAEFLGG - ARNEADFVTDQVSHRMPPRSRKFCVLVRA --	-VTASES	235					

DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGF-beta.
 DR Pfam; PF0019; TGF-beta; 1.
 DR PRINTS; PRO0438; GFCYSKNOT.
 DR PRINTS; PRO0669; INHIBINA.
 DR PRODOM; PD000357; TGF-beta; 1.
 DR SMART; SM00204; TGFbeta; 1.
 DR PROSITE; PS00250; TGF_beta; 1.
 DR Glycoprotein.
 KW
 NON_TER 1 1
 FT NON_TER 289 289
 SEQUENCE 289 AA; 33599 MW; 99E175C7DBC3C58B CRC64;

Query	Match	Score	Length
Best Local Similarity	24.28;	24.26;	5;
Matches 106; Conservative	31.78;	Pred. No. 2.4e-29;	
Mismatches	54;	Indels	78;
Gaps	11;		
Qy 16 FDSVMSLSDKEELVGAELRLFR-----QAPSAPWGPPAGPLH----VQLFPCLSLPL- 2 FTVSTMPEEEWTAAELRLFKDLDDEHHIVKRHALHDRESLKPHYMQRINVYHLKPVA 61			
-W 62 -----LLDARTLDPQGAPPAGLWYFDWQGLR--HOPWKQCLCELAQKGELDAGE 110			
Db 62 RNRDTIKLIDTRLVDRN--ASWSFSDVRPAMRWLEEPENKNGLEI----+L--- 109			
Qy 111 AFARARGPQQPPPDLRLSLGFGRVRPQPQEALVVFTRSQRKNLFAEMREQGSAEAAG 170			
Db 110 IDSRGR----PSPNHHHVRYVTRADPSKVEEL----ENEEDRWFQTRPQITYSDDG 159			
Qy 171 PGAGAEGSWPPSGAPDARPLPSPPRRRTAFASRHG---KHGKKSRLRCSKKPLH 226			
Db 160 -----RTKRSPSSSSSGRQKRGKRLKANCRRHELY 192			
Qy 227 VNFKELGDDWIAPLEYEAYHCEGYCDFPPLRSHLEPTNAIIOTLMNSNDPGSTPPSCC 286			
Db 193 VDFSDVWNWDWIVAPAGYQAYCGRGCPFPPLAENNTNHAIVOTFLVNNSVNPALVPKACC 252			
Qy 287 VPTKLTPISILYIDAGNNVYVKQYEDMVYESCGC 320			
Db 253 VPTELSAISMLYLDYEKVKVLKNYQDMVVECCGC 286			

Search completed: October 3, 2002, 15:45:37
 Job time: 4.13 sec